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#4

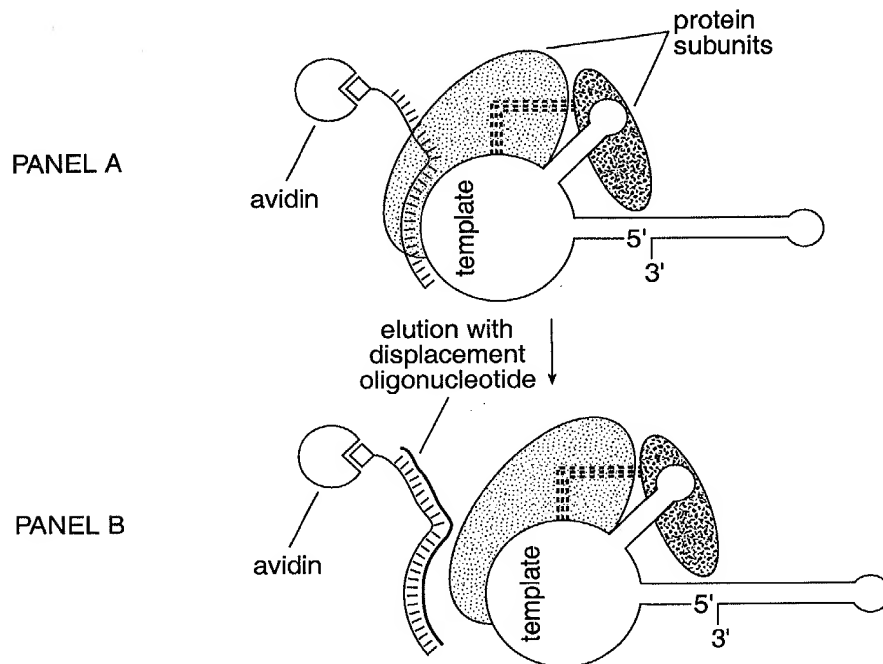


FIG. 1

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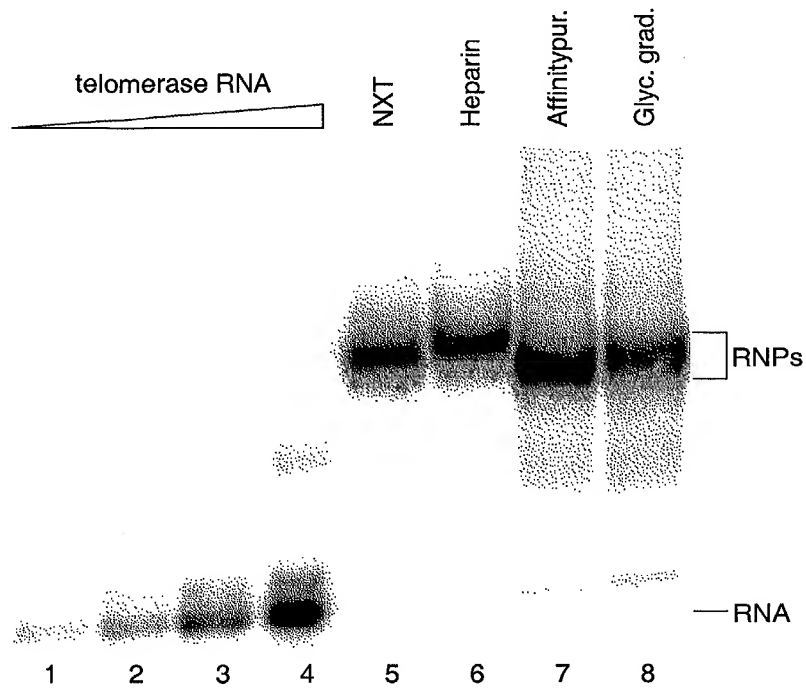


FIG. 2

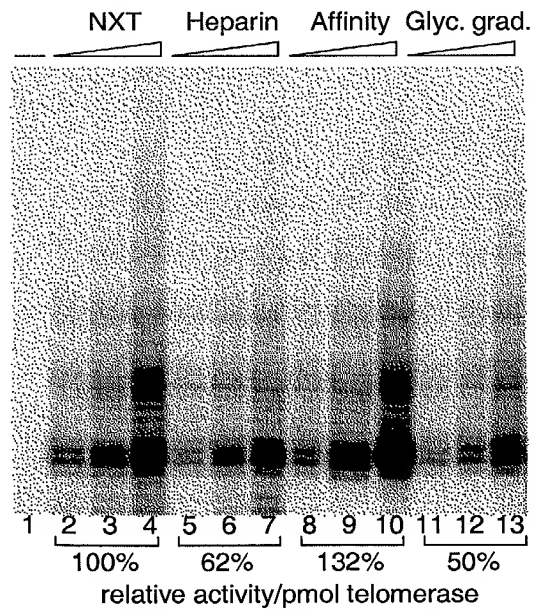


FIG. 3

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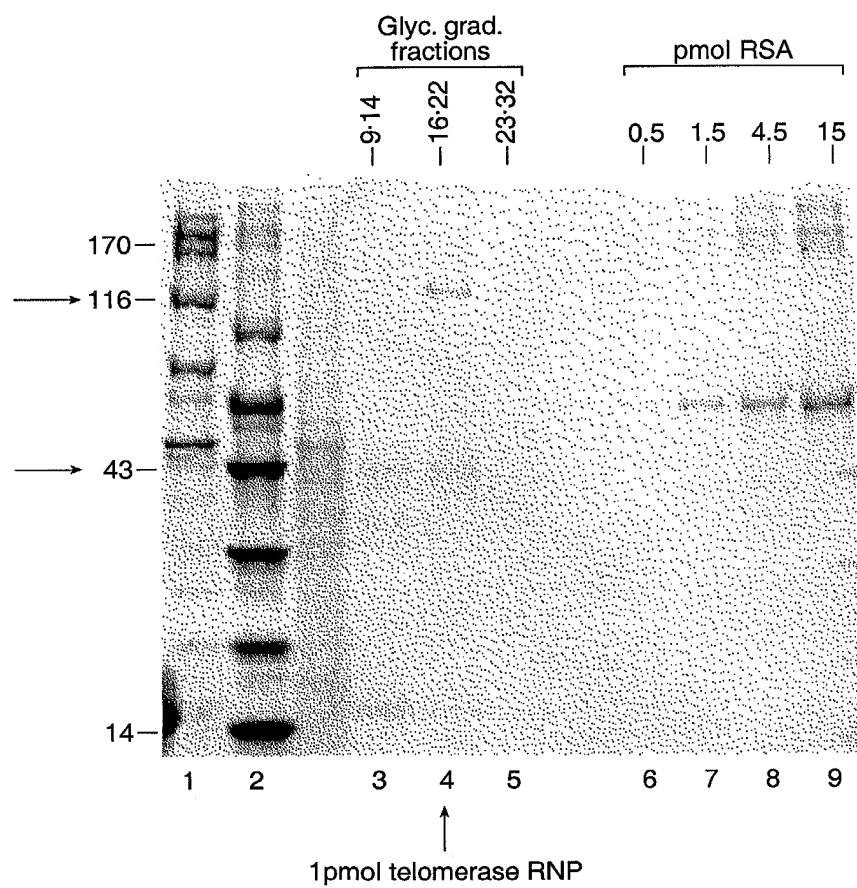


FIG. 4

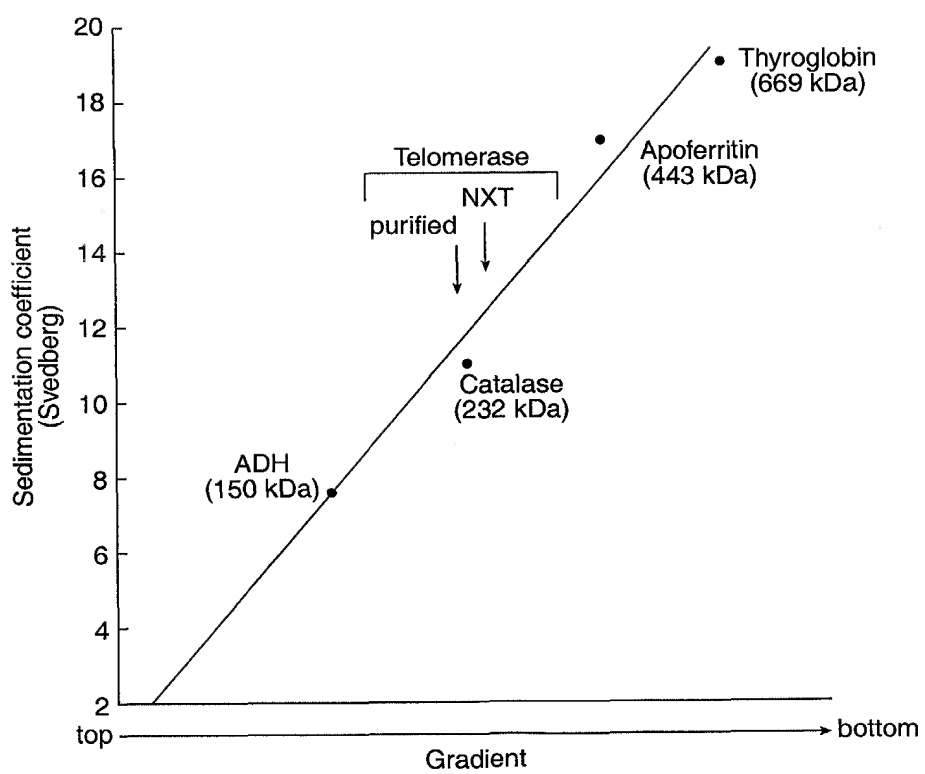
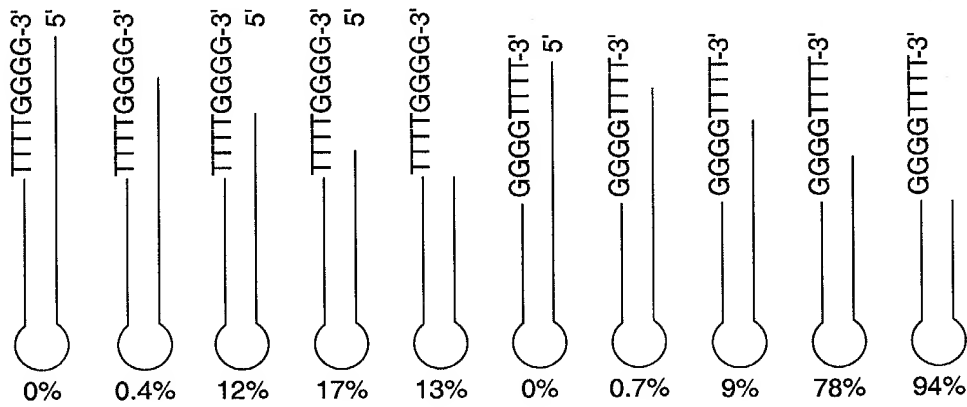
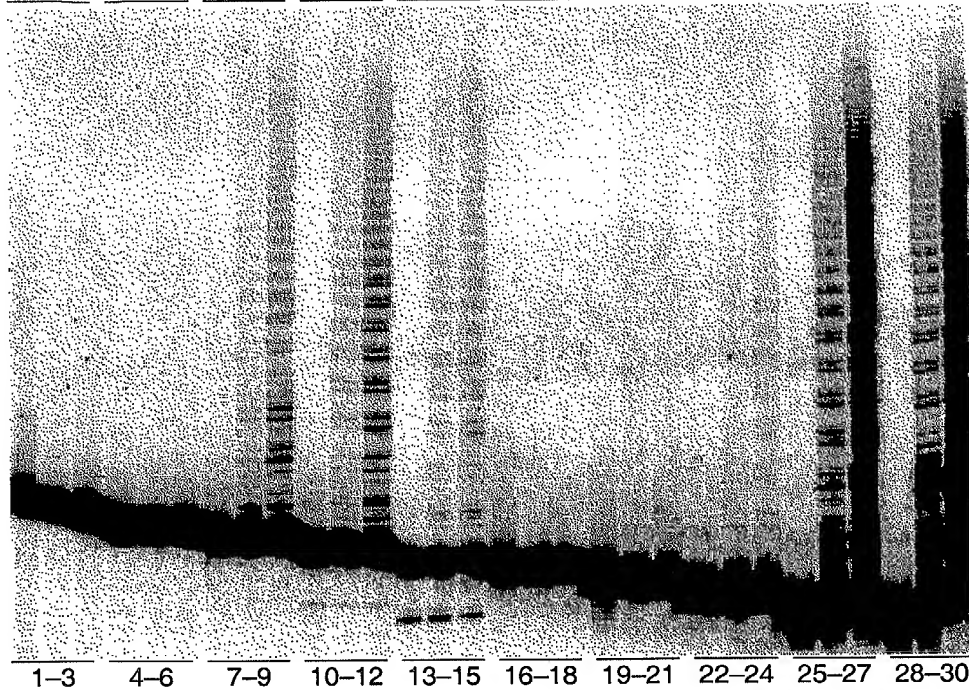


FIG. 5

Telomerase:

+	+	+	+	+	+	+	+	+	+
+	+	+	+	+	+	+	+	+	+
-	+	+	-	+	+	-	+	+	-
+	+	+	+	+	+	+	+	+	+



% primer extended

FIG. 6

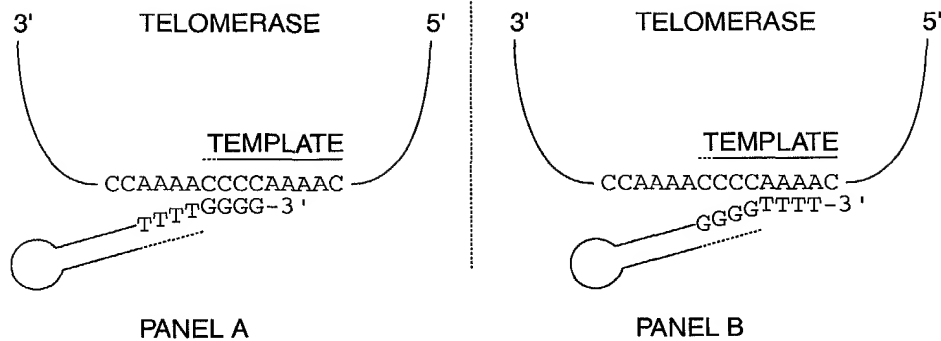


FIG. 7

1	CCCCAAAACC	CCAAAACCCC	AAAACCCCTA	TAAAAAAGA	AAAAATTGAG
51	GTAGTTTAGA	AATAAAATAT	TATTCCTGCA	CAAATGGAGA	TGGATATTGA
101	TTTGGATGAT	ATAGAAAATT	TACTTCCTAA	TACATTCAAC	AAGTATAGCA
151	GCTCTTGTAG	TGACAAGAAA	GGATGCAAAA	CATTGAAATC	TGGCTCGAAA
201	TCGCCTTCAT	TGACTATTCC	AAAGTTGCAA	AAACAATTAG	AGTTCTACTT
251	CTCGGATGCA	AATCTTTATA	ACGATTCTTT	CTTGAGAAAA	TTAGTTTTAA
301	AAAGCGGAGA	GCAAAGAGTA	GAAATTGAAA	CATTACTAAT	GTTTAAATAA
351	AATCAGGTAA	TGAGGATTAT	TCTATTTT	AGATCACTTC	TTAAGGAGCA
401	TTATGGAGAA	AATTACTTAA	TACTAAAAGG	TAAACAGTTT	GGATTATTTC
451	CCTAGCCAAC	AATGATGAGT	ATATTAAATT	CATATGAGAA	TGAGTCAAAG
501	GATCTCGATA	CATCAGACTT	ACCAAAGACA	AACTCGCTAT	AAAACGCAAG
551	AAAAAGTTTG	ATAATCGAAC	AGCAGAAGAA	CTTATTGTCAT	TTACTATTTCG
601	TATGGGTTTT	ATTACAATTG	TTTTAGGTAT	CGACGGTGAA	CTCCCGAGTC
651	TTGAGACAAT	TGAAAAAGCT	GTTTACAAC	GAAGGAATCG	CAGTTCTGAA
701	AGTTCTGATG	TGTATGCCAT	TATTTTGTGA	ATTAATCTCA	AATATCTTAT
751	CTCAATTTAA	TGGATAGCTA	TAGAAACAAA	CCAAATAAAC	CATGCAAGTT
801	TAATGGAATA	TACGTTAAAT	CCTTTGGGAC	AAATGCACAC	TGAATTTATA
851	TTGGATTCTT	AAAGCATAGA	TACACAGAA	GCTTTAGAGA	CTGATTTAGC
901	TTACAACAGA	TTACCTGTTT	TGATTACTCT	TGCTCATCTC	TTATATCTTT
951	AAAAGAAGCA	GGCGAAATGA	AAAGAAGACT	AAAGAAAGAG	ATTTCAAAT
1001	TTGTTGATTC	TTCTGTAACC	GGAATTAACA	ACAAGAATAT	TAGCAACGAA
1051	AAAGAAGAAG	AGCTATCACA	ATCCTGATTC	TTAAAGATTT	CAAAAATPCC
1101	AGGTAAGAGA	GATACATTCA	TTAAAATTCA	TATATTATAG	TTTTTCATTT
1151	CACAGCTGTT	ATTTTCTTTT	ATCTTAACAA	TATTTTGTGA	TTAGCTGGAA
1201	GTAAAAAGTA	TCAAATAAGA	GAAGCGCTAG	ACTGAGGTAA	CTTAGCTTAT
1251	TCACATTCAT	AGATCGACCT	TCATATATCC	AATACGATGA	TAAGGAAACA
1301	GCAGTCATCC	GTTTTAAAAA	TAGTGCTATG	AGGACTAAAT	TTTTTAGAGTC
1351	AAGAAATGGA	GCCGAAATCT	TAATCAAAAA	GAATTGCGTC	GATATTGCAA
1401	AAGAATCGAA	CTCTAAATCT	TTCGTTAATA	AGTATTACCA	ATCTTGATTG
1451	ATTGAAGAGA	TTGACGAGGC	AACTGCACAG	AAGATCATT	AAGAAATAAA
1501	GTAACCTTTT	TTAATTAGAG	AATAAACTAA	ATTACTAATA	TAGAGATCAG
1551	CGATCTTCAA	TTGACGAAAT	AAAAGCTGAA	CTAAAGTTAG	ACAATAAAAA
1601	ATACAAACCT	TGGTCAAAAT	ATTGAGGAAG	GAAAAAGAAG	CCAGTTAGCA
1651	AAAGAAAAAA	TAAGGCAATA	AATAAAATGA	GTACAGAAGT	GAAGAAATAA
1701	AAGATTTATT	TTTTTCAATA	ATTTATTGAA	AAGAGGGGTT	TTGGGGTTTTT
1751	GGGGTTTTTG	GG			

FIG. 11

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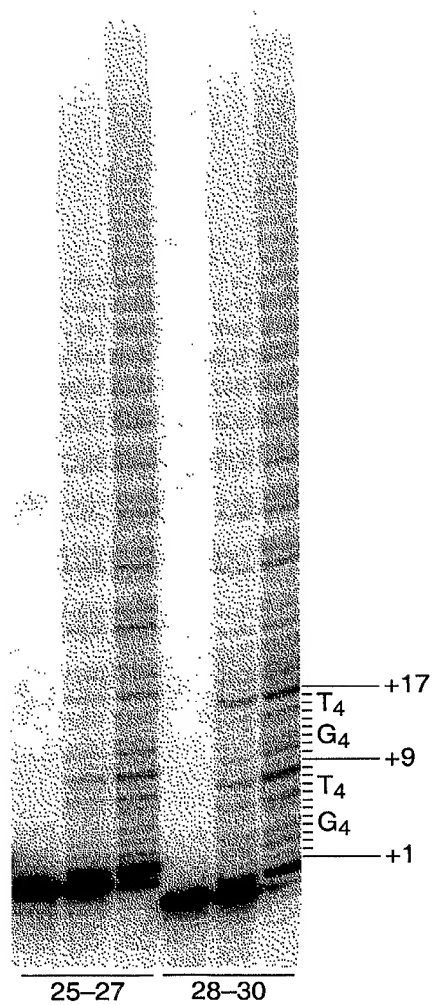


FIG. 8

1 AAAACCCCAA AACCCCAAAA CCCCTTTT TAG AGCCCTGCAG TTGGAAATAT
 51 AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA
 101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCACTCAGC
 151 TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAACGTTG TACTCTTGGA
 201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT
 251 TTAGAAGATA TAAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG
 301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT
 351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAACCTCTT
 401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTCA
 451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCAA
 501 CTCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG
 551 ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA
 601 GCGAACTTCT GAAGGAAGTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG
 651 ATCATTTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA
 701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAAT ACAATGTCAA
 751 GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGGAATA
 801 ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT TAATAGAAAT
 851 AACCATTCTT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTT
 901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA
 951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCCTACATG
 1001 CTTGAGAAAG TCAAAGATTT TAACCTCAAC TACTATTTAA CAAAATCTTG
 1051 TCCCTCTTCCA GAAAATTGGC GGAACGGAA ACAAAAAATC GAAAACCTGA
 1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC
 1151 TACACAAC TG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTCTA
 1201 CAATATAC TC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC
 1251 AAAAGAAAAGT TAAGAAATAT GTGGAACATA ACAAGCATGA ACTCATTCAC
 1301 AAAAATTTAT TGCCTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA
 1351 GGTTGAGACC TCTGCAAAGC ATTTTATTTA TTTTGATCAC GAAAACATCT
 1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGCTCG
 1451 CTGATTAGAT GATTTTCTTA TGTCACCGAG CAACAGAAAA GTTACTCCAA
 1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA
 1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT
 1601 GAAGAATGGA AAAAGTCGCT TGGATTTGCA CCTGGAAAAC TCAGACTAAT
 1651 ACCGAAGAAA ACTACTTTCC GTCCAATTAT GACTTTCAAT AAGAAGATTG
 1701 TAAATTCAGA CCGGAAGACT ACAAAATTAA CTACAAATAC GAAGTTATTG
 1751 AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC
 1801 TTTTGGAATC GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG
 1851 AGTTTGTTTG CAAATGGAAG CAAGTTGGAC AACCAAAAC CTCTTTGCA
 1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAATATC
 1951 AACATTCCTA AAACTACTA AATTACTTTC TTCAGATTTC TGGATTATGA
 2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC
 2051 TTTAGAAAAG AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT
 2101 TGCATTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGT CTTGAAAATG
 2151 AACAAAATGA CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAAGCAA
 2201 AGAAATTATT TTAAGAAAGA TAACTTACTT CAACCAGTCA TTAATATTTG
 2251 CCAATATAAT TACATTAACT TTAATGGGAA GTTTTATAAA CAAACAAAAG
 2301 GAATTCCTCA AGGTCCTTGA GTTTCATCAA TTTTGTATC ATTTTATTAT
 2351 GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA

FIG. 9

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2401	CCCTGAAAAAT	CCAAATGTTA	ATCTTCTAAT	GAGACTTACA	GATGACTATC
2451	TTTTGATTAC	AACTCAAGAG	AATAATGCAG	TATTGTTTAT	TGAGAAACTT
2501	ATAAACGTAA	GTCGTGAAAA	TGGATTAAAA	TTCAATATGA	AGAAACTACA
2551	GACTAGTTTT	CCATTAAGTC	CAAGCAAATT	TGCAAAATAC	GGAATGGATA
2601	GTGTTGAGGA	GCAAAATATT	GTTCAAGATT	ACTGCGATTG	GATTGGCATC
2651	TCAATTGATA	TGAAAACTCT	TGCTTTAATG	CCAAATATTA	ACTTGAGAAT
2701	AGAAGGAATT	CTGTGTACAC	TCAATCTAAA	CATGCAAAACA	AAGAAAGCAT
2751	CAATGTGGCT	CAAGAAGAAA	CTAAAGTCGT	TTTTAATGAA	TAACATTACC
2801	CATTATTTTA	GAAAGACGAT	TACAACCGAA	GACTTTGCGA	ATAAAACTCT
2851	CAACAAGTTA	TTTATATCAG	GCGGTTACAA	ATACATGCAA	TGAGCCAAAG
2901	AATACAAGGA	CCACTTTAAG	AAGAACTTAG	CTATGAGCAG	TATGATCGAC
2951	TTAGAGGTAT	CTAAATTTAT	ATACTCTGTA	ACCAGAGCAT	TCTTTAAATA
3001	CCTTGTGTGC	AATATTAAGG	ATACAAATTT	TGGAGAGGAG	CATTATCCAG
3051	ACTTTTTCCCT	TAGCACACTG	AAGCACTTTA	TTGAAATATT	CAGCACAAAA
3101	AAGTACATTT	TCAACAGAGT	TTGCATGATC	CTCAAGGCAA	AAGAAGCAAA
3151	GCTAAAAAGT	GACCAATGTC	AATCTCTAAT	TCAATATGAT	GCATAGTCGA
3201	CTATTTCTAAC	TTATTTTGGG	AAGTTAATTT	TCAATTTTTG	TCTTATATAC
3251	TGGGGTTTTG	GGGTTTTTGG	GTTTTTGGGG		

FIG. 9
(CONTINUED)

1	MEVDVDNQAD	NHGIHSALKT	CEEIKEAKTL	YSWIQKVIRC	RNQSQSHYKD
51	LEDIKIFAQT	NIVATPRDYN	EEDFKVIARK	EVFSTGLMIE	LIDKCLVELL
101	SSSDVSDRQK	LQCFGFQLKG	NQLAKTHLLT	ALSTQKQYFF	QDEWNQVRAM
151	IGNELFRHLY	TKYLIFQRTS	EGTLVQFCGN	NVFDHLKVND	KFDKKQKGA
201	ADMNEPRCCS	TCKYNVKNEK	DHFLNNINVP	NWNNMKSRT	IFYCTHFNRN
251	NQFFKKHEFV	SNKNNISAMD	RAQTIFTNIF	RFNRIRKKLK	DKVIEKIAM
301	LEKVKDFNFN	YYLTKSCPLP	ENWRERKQKI	ENLINKTREE	KSKYEEELFS
351	YTTDNKCVTQ	FINEFFYNIL	PKDFLTGRNR	KNFQKKVKKY	VELNKHელი
401	KNLLLEKINT	REISWMQVET	SAKHFYFDH	ENIYVLWKL	RWIFEDLVVS
451	LIRCFYVTE	QOKSYSKTY	YRKNWVIM	KMSIADLKKE	TLAEVQKEV
501	EEWKSLGFA	PGKLRLIPK	TTFRPIMTFN	KKIVNSDRKT	TKLTNTKL
551	NSHMLKTLK	NRMFKDPFGF	AVFNYDDVMK	KYEEFVCKWK	QVGQPKLFFA
601	TMDIEKCYDS	VNREKLSTFL	KTTKLLSSDF	WIMTAQILKR	KNNIVIDSKN
651	FRKKEMKDYF	RQKFQKIALE	GGQYPTLFSV	LENEQNDLNA	KKTLIVEAKQ
701	RNYFKKDNLL	QPVINICQYN	YINFNGKFYK	QTKGIPQGLC	VSSILSSFY
751	ATLEESSLGF	LRDESMNPEN	PNVNLLMRLT	DDYLLITTQE	NNAVLFIEKL
801	INVSRENGFK	FNMKKLQTSF	PLSPSKFAKY	GMDSVEEQNI	VQDYCDWIGI
851	SIDMKTLALM	PNINLRIEGI	LCTLNLMQ	KKASMWLKKK	LKSFLMNNIT
901	HYFRKTIITE	DFANKTLNKL	FISGGYKYM	CAKEYKDHFK	KNLAMSSMID
951	LEVSKIIYSV	TRAFFKYLVC	NIKDTIFGEE	HYPDFFLSTL	KHFIEIFSTK
1001	KYIFNRVCM	LKAKEAKLKS	DQCQSLIQYD	A	

FIG. 10

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CCCCAAAACCCCAAAACCCCAAAACCCCTATAAAAAAGAAAAAATTGAGGTAGTTTAGA
 1 -----+-----+-----+-----+-----+-----+ 60
 GGGGTTTTGGGGTTTTGGGGTTTTGGGGATATTTTTTCTTTTTTAACCTCCATCAAATCT

a P Q N P K T P K P L * K K K K L R * F R -
 b P K T P K P Q N P Y K K R K N C G S L E -
 c P K P Q N P K T P I K K E K I E V V * K -

AATAAAATATTATTCCCGCACAAATGGAGATGGATATTGATTTGGATGATATAGAAAATT
 61 -----+-----+-----+-----+-----+ 120
 TTATTTTATAATAAGGGCGTGTTCACCTCTACCTATAACTAAACCTACTATATCTTTTAA

a N K I L F P H K W R W I L I W M I * K I -
 b I K Y Y S R T N G D G Y C F G C Y R K F -
 c * N I I P A Q M E M D I D L D D I E N L -

TACTTCCTAATACATTCAACAAGTATAGCAGCTCTTGTAGTGACAAGAAAGGATGCAAAA
 121 -----+-----+-----+-----+-----+ 180
 ATGAAGGATTATGTAAGTTGTTTCATATCGTCGAGAACATCACTGTTCTTTCCTACGTTTT

a Y F L I H S T S I A A L V V T R K D A K -
 b T S * Y I Q Q V * Q L L * * Q E R M Q N -
 c L P N T F N K Y S S S C S D K K G C K T -

CATTGAAATCTGGCTCGAAATCGCCTTCATTGACTATTCCAAAGTTGCAAAAACAATTAG
 181 -----+-----+-----+-----+-----+ 240
 GTAACCTTTAGACCGAGCTTTAGCGGAAGTAACTGATAAGGTTTCAACGTTTTTGTTAATC

a H C N L A R N R L H C L F Q S C K N N * -
 b I E I W L E I A F I D Y S K V A K T I R -
 c L K S G S K S P S L T I P K L Q K Q L E -

AGTTCTACTTCTCGGATGCAAAATCTTTATAACGATTCTTTCTTGAGAAAATTAGTTTTAA
 241 -----+-----+-----+-----+-----+ 300
 TCAAGATGAAGAGCCTACGTTTAGAAATATTGCTAAGAAAGAACTCTTTTAATCAAAATT

a S S T S R M Q I F I T I L S C E N * F * -
 b V L L L G C K S L * R F F L E K I S F K -
 c F Y F S D A N L Y N D S F L R K L V L K -

AAAGCGGAGAGCAAAGAGTAGAAATTGAAACATTACTAATGTTTAAATAAAATCAGGTAA
 301 -----+-----+-----+-----+-----+ 360
 TTTTCGCTCTCGTTTCTCATCTTTAACTTTGTAATGATTACAAATTTATTTTAGTCCATT

a K A E S K E * K L K H Y * C L N K I R * -
 b K R R A K S R N C N I T N V * I K S G N -
 c S G E Q R V E I E T L L M F K * N Q V M -

TGAGGATTATCTATTTTTTTAGATCACTTCTTAAGGAGCATTATGGAGAAAATTACTTAA
 361 -----+-----+-----+-----+-----+ 420
 ACTCCTAATAAGATAAAAAATCTAGTGAAGAATTCCTCGTAATACCTCTTTTAATGAATT

a C G L F Y F L D H F L R S I M E K I T * -
 b E D Y S I F * I T S * G A L W R K L L N -
 c R I I L F F R S L L K E H Y G E N Y L I -

FIG. 12

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TACTAAAAGGTAAACAGTTTGGATTATTTCCCTAGCCAACAATGATGAGTATAT'TAAATT
421 -----+-----+-----+-----+-----+-----+-----+ 480
ATGATTTTCCATTTGTCAAACCTAATAAAGGGATCGGTTGTTACTACTCATATAATTTAA

a Y * K V N S L D Y F P S Q Q C C V Y * I -
b T K R * T V W I I S L A N N D E Y I K F -
c L K G K Q F G L F P * P T M M S I L N S -

CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAGACAAACTCGCTAT
481 -----+-----+-----+-----+-----+-----+ 540
GTATACTCTTACTCAGTTTCCTAGAGCTATGTAGTCTGAATGGTTTCTGTTTGAGCGATA

a H M R M S Q R I S I H Q T Y Q R Q T R Y -
b I C E C V K G S R Y I R L T K D K L A I -
c Y E N E S K D L D T S D L P K T N S L * -

AAAACGCAAGAAAAAGTTTGATAATCGAACAGCAGAAGAACTTATTGCATTTACTATTCG
541 -----+-----+-----+-----+-----+-----+ 600
TTTTGCGTTCTTTTTCAAACATATTAGCTTGTCTCTTCTGAATAACGTAAATGATAAGC

a K T Q E K V C * S N S R R T Y C I Y Y S -
b K R K K K F D N R T A E E L I A F T I R -
c N A R K S L I I E Q Q K N L L H L L F V -

TATGGGTTTATTACAATTGTTTTAGGTATCGACGGTGAACCTCCGAGTCTTGAGACAAT
601 -----+-----+-----+-----+-----+-----+ 660
ATACCCAAAATAATGTTAACAAAATCCATAGCTGCCACTTGAGGGCTCAGAACTCTGTTA

a Y G F Y Y N C F R Y R R C T P E S C D N -
b M G F I T I V L G I D G E L P S L E T I -
c W V L L Q L F * V S T V N S R V L R Q L -

TGAAAAAGCTGTTTACAACTGAAGGAATCGCAGTTCTGAAAGTTCTGATGTGTATGCCAT
661 -----+-----+-----+-----+-----+-----+ 720
ACTTTTTTCGACAAATGTTGACTTCCTTAGCGTCAAGACTTTCAAGACTACACATACGGTA

a C K S C L Q L K E S Q F C K F * C V C H -
b E K A V Y N C R N R S S E S S D V Y A I -
c K K L F T T E G I A V L K V L M C M P L -

TATTTTGTGAATTAATCTCAAATATCTTATCTCAATTTAATGGATAGCTATAGAAACAAA
721 -----+-----+-----+-----+-----+-----+ 780
ATAAAACACTTAATTAGAGTTTATAGAATAGAGTTAAATTACCTATCGATATCTTTGTTT

a Y F V N * S Q I S Y L N L M D S Y R N K -
b I L C I N L K Y L I S I * W I A I E T N -
c F C E L I S N I L S Q F N G * L * K Q T -

CCAAATAAACCATGCAAGTTTAAATGAATATACGTAAATCCTTTGGGACAAATGCACAC
781 -----+-----+-----+-----+-----+-----+ 840
GGTTTATTTGGTACGTTCAAATTACCTTATATGCAATTTAGGAAACCCTGTTTACGTGTG

a P N K P C K F N G I Y V K S F G T N A H -
b Q I N H A S L M E Y T L N P L G Q M H T -
c K * T M Q V * W N I R * I L W D K C T L -

TGAATTTATATTGGATTCTTAAAGCATAGATACACAGAATGCTTTAGAGACTGATTTAGC
841 -----+-----+-----+-----+-----+-----+ 900
ACTTAAATATAACCTAAGAATTTCTGATCTATGTGTCTTACGAAATCTCTGACTAAATCG

a C I Y I G F L K H R Y T E C F R D C F S -
b E F I L D S * S I D T Q N A L E T D L A -
c N L Y W I L K A * I H R M L * R L I * L -

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FIG. 12
(CONTINUED)

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TTACAACAGATTACCTGTTTTGATTACTCTTGCTCATCTCTTATATCTTTAAAAGAAGCA
 901 -----+-----+-----+-----+-----+ 960
 AATGTTGTCTAATGGACAAAACCTAATGAGAACCAGTAGAGAATATAGAAATTTTCTTCGT

 a L Q Q I T C F D Y S C S S L I S L K E A -
 b Y N R L P V L I T L A H L L Y L * K K Q -
 c T T D Y L F C L L L L I S Y I F K R S R -

 GGCGAAATGAAAAGAAGACTAAAGAAAGAGATTTCAAAATTTGTTGATTCTTCTGTAACC
 961 -----+-----+-----+-----+-----+ 1020
 CCGCTTTACTTTTCTTCTGATTCTTTCTCTAAAGTTTTAAACAATAAGAAGACATTGG

 a G E M K R R L K K E I S K F V D S S V T -
 b A K C K E D * R K R F Q N L L I L L * P -
 c R N E K K T K E R D F K I C C F F C N R -

 GGAATTAACAACAAGAATATTAGCAACGAAAAAGAAGAGCTATCACAATCCTGATTC
 1021 -----+-----+-----+-----+-----+ 1080
 CCTTAATTGTTGTTCTTATAATCGTTGCTTTTTCTTCTCTCGATAGTGTAGGACTAAG

 a G I N N K N I S N E K E E E L S Q S C F -
 b E L T T R I L A T K K K K S Y H N P D S -
 c N * Q Q E Y * Q R K R R R A I T I L I L -

 TTAAAGATTTCAAAAATTCAGGTAAGAGAGATACATTCAATTAATTCATATATTATAG
 1081 -----+-----+-----+-----+-----+ 1140
 AATTTCTAAAGTTTAAAGGTCCATTCTCTCTATGTAAGTAATTTAAAGTATATAATATC

 a L K I S K I P G K R D T F I K I H I L * -
 b * R F Q K F Q V R E I H S L K F I Y Y S -
 c K D F K N S R * E R Y I H * N S Y I I V -

 TTTTTCATTTACAGCTGTTATTTTCTTTTATCTTAACAATATTTTGTGATTAGCTGGAA
 1141 -----+-----+-----+-----+-----+ 1200
 AAAAAGTAAAGTGTGACAATAAAAGAAAATAGAATTGTTATAAAAACTAATCGACCTT

 a F F I S Q L L F S F I L T I F F D * L E -
 b F S F H S C Y F L L S * Q Y F L I S W K -
 c F H F T A V I F F Y L N N I F C L A G S -

 GTAAAAAGTATCAAATAAGAGAAGCGCTAGACTGAGGTAACCTAGCTTATTCACATTCAT
 1201 -----+-----+-----+-----+-----+ 1260
 CATTTTTTCATAGTTTATTCTCTTCGCGATCTGACTCCATTGAATCGAATAAGTGTAAAGTA

 a V K S I K * E K R * T E V T * L I H I H -
 b * K V S N K R S A R L R * L S L F T F I -
 c K K Y Q I R E A L D C G N L A Y S H S * -

 AGATCGACCTTCATATATCCAATACGATGATAAGGAAACAGCAGTCATCCGTTTTAAAAA
 1261 -----+-----+-----+-----+-----+ 1320
 TCTAGCTGGAAGTATATAGGTTATGCTACTATTCTTTGTCGTCAGTAGGCAAAATTTTT

 a R S T F I Y P I R C * G N S S H P F * K -
 b D R P S Y I Q Y D D K E T A V I R F K N -
 c I D L H I S N T M I R K Q Q S S V L K I -

 TAGTGCTATGAGGACTAAATTTTGTAGAGTCAAGAAATGGAGCCGAAATCTTAATCAAAAA
 1321 -----+-----+-----+-----+-----+ 1380
 ATCAGGATACTCCTGATTTAAAAATCTCAGTTCTTTACCTCGGCTTTAGAATTAGTTTTT

 a * C Y E D * I F R V K K W S R N L N Q K -
 b S A M R T K F L E S R N G A E I L I K K -
 c V L C G L N F * S Q E M E P K S * S K R -

FIG. 12
(CONTINUED)

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GAATTGCGTCGATATTGCAAAAGAATCGAACTCTAAATCTTTTCGTTAATAAGTATTACCA
 1381 -----+-----+-----+-----+-----+ 1440
 CTTAACGCAGCTATAACGTTTTCTTAGCTTGAGATTTAGAAAGCAATTATTCATAATGGT

a E L R R Y C K R I E L * I F R * * V L P -
 b N C V D I A K E S N S K S F V N K Y Y Q -
 c I A S I L Q K N R T L N L S L I S I T N -

ATCTTGATTGATTGAAGAGATTGACGAGGCAACTGCACAGAAGATCATTAAAGAAATAAA
 1441 -----+-----+-----+-----+-----+ 1500
 TAGAACTAACTAACTTCTCTAAGTCTCCGTTGACGTGTCTTCTAGTAATTTCTTTATTT

a I L I D C R D * R G N C T E D H * R N K -
 b S C L I E E I D E A T A Q K I I K E I K -
 c L D C L K R L T R Q L H R R S L K K * S -

GTAACCTTTTATTAATTAGAGAATAAACTAAATTACTAATATAGAGATCAGCGATCTTCAA
 1501 -----+-----+-----+-----+-----+ 1560
 CATTGAAAATAATTAATCTCTTATTTGATTTAATGATTATATCTCTAGTCGCTAGAAGTT

a V T F I N * R I N * I T N I E I S D L Q -
 b * L L L I R E * T K L L I * R S A I F N -
 c N F Y * L E N K L N Y * Y R D Q R S S I -

TTGACGAAATAAAAGCTGAACTAAAGTTAGACAATAAAAAATACAAACCTTGGTCAAAT
 1561 -----+-----+-----+-----+-----+ 1620
 AACTGCTTTATTTTCGACTTGATTTCATCTGTTATTTTTATGTTTGAACCAAGTTTAA

a L T K * K L N * S * T I K N T N L G Q N -
 b C R N K S C T K V R Q * K I Q T L V K I -
 c D E I K A E L K L D N K K Y K P W S K Y -

ATTGAGGAAGGAAAAGAAGACCAGTTAGCAAAAGAAAAAATAAGGCAATAAATAAAATGA
 1621 -----+-----+-----+-----+-----+ 1680
 TAACTCCTTCCTTTCTCTGGTCAATCGTTTCTTTTATTCCGTTATTTATTTTACT

a I E E G K E D Q L A K E K I R Q * I K C -
 b L R K E K K T S * Q K K K * G N K * N E -
 c C G R K R R P V S K R K N K A I N K M S -

GTACAGAAGTGAAGAAATAAAAGATTTATTTTTTTCAATAATTTATTGAAAAGAGGGGTT
 1681 -----+-----+-----+-----+-----+ 1740
 CATGTCTTCACTTCTTTATTTTCTAAATAAAAAAAGTTATTAAATAACTTTTCTCCCCAA

a V Q K C R N K R F I F F N N L L K R G V -
 b Y R S E E I K D L F F S I I Y C K E G F -
 c T E V K K * K I Y F F Q * F I E K R G F -

TTGGGGTTTTGGGGTTTTGGGG
 1741 -----+-----+-----+-----+-----+ 1762
 AACCCCAAACCCCAAACCC

a L G F W G F G -
 b W G F G V L G -
 c G V L G F W -

FIG. 12
 (CONTINUED)

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FIG. 13

+

+

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798 EKLINVSRENGFKFNMKK.LQTSFPLSPSKFAKYGMDSVEEQNIVQDYCD 846
PGDELPSMQKLLQEKGLGGG..TDFPYECIDEWTKNKNTHVD 617
 847 WIGISIDMKTLALMPNINLRIEGILCTLNLMQTKKASMWLKKKLSFLM 896
 618 NIVILSDMMIAEGYSDINVRGSSIVNSI.....KKYKDEVN 653
 897 NNITHYFRKTITTEDFANKTLNKLFISSGGYKYMQCAKEYKD.HFKKNLAM 945
 654 PNIKIF...AVDLEGYG.....KCLNLGDEFNENNYIKIFGM 687
 946 SSMIDLEVSKIIYSVTRAFFKYLVCNIKDTIFGEEHYDPDFLSTLKHFI 995
 688 SDSI.....LKFISAKQGA.....NMVE 706
 996 IFSTKKYIFNRVC 1008
 707 VI..KNFALQKIG 717

FIG. 13
(CONTINUED)

132 LSTQKQYFFQDEWNQVRAMIGNEL.FRHLTYKYLIFQRTSE..GTLVQFC 178
 1 MSRRNQ.....KKPQAPIGNETNLDVFLQNLLEVYKSQIEHYKTQQQQI 43
 179 GNNVFDHLKVNDKFDKKQKGAADMNEPRCCSTCKYNVKNKEDHFLNNIN 228
 44 KEEDLKLKFKNQDQDGNSGNDDDEE.....NNSNKQQELLRRVN 84
 229 VPNNWNMKSRTTRIFYCTHFNRRNQFFKKHEFVSNNKNNISAMDRAQTIFTN 278
 85QIKQVQLIKK...VGSKEKDLNLDENENKN 114
 279 IFRFNIRKKLKDVKIEKIAMLEKVKDFNFNYLTKSCPLPENWRERKQ 328
 115 GLSEQQVKEEQRLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRRETDY 164
 329 KIENLINKTREETSKYEEELFSYTTDNKCVTQFINE.FFYNILPKDFTLG 377
 165 DTEKWFEISHDQK.....NYVSIYANQKTSYCWWLKDYFNK 200
 378 RNRKNFQKKVKKYVELNKHLEIHNKLLLEKINTREISWMQVETSAKHFFY 427
 201 NNYDHLNVSINRLE..TEAEFYAFDDFSQTIKLTNNSYQTVNID..... 242
 428 FDHENIYVLWKLLRWI..FEDLVVSLIRCFYVTEQOKSYSKTYYYRKNI 475
 243 VNFDNNLCILALLRFLSLERFNILNIRSSY..TRNQYNFEKIGELLETI 290
 476 WDVIMKMSIADLKKETLAEVQKEVEEWKSLGFAPGKLRLIPKKTTFRP 525
 291 FAVVFSHR.....HLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQ 330
 526 IMTFNKKIVNSDRKTTKLTTNTKLLNSHMLKTLKNRMFKDPFGFAVFNY 575
 331 VYSFSTDLKLVD..TNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENL 378

FIG. 14

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00220 05299760

[illegible]

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FIG. 15

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1 MEMDIDLDDIENL.....LPNTFNKYSSSCDDKKGCKTLKSGSKSPS... 42
  | : | . . . | | | . . . | : | | . . . . . | | | . . .
491 IELAIAKIIVNKNLDEIKGHTAIFSDVSGSMSTSMSSGGAKKYGSVRTCLEC 540

43 .LTIPKLQKQ.....LEFYFSDANLYNDSFLRKLVLKSGEQRVEIETLL 85
  | : | . . . | | | . . . | : | | . . . . . | | | . . .
541 ALVLGLMVKQRCEKSSFYIFSSPSSQCNKCYL.EVDLPGDEL RPSMQKLL 589

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FIG. 16

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telomerase p43 LQKQLEFYFSDANLYNDSFLRKLVLKSGEQRVEIETLLM
human La ICHQIEYFYFGDFNLPRDKFLKEQI.KLDEGWVPLEIMIK
Xenopus LaA ICEQIEYFYFGDHNLPDKFKKQOI.LLDDGWVPLETMIK
Drosophila La ILRQVEYFYGDANLNDRDKFIREQIGKNEDGWVPLSVLVT
S. c. Lhplp CLKQVEFYFSEFNFPYDRFLRTTAEK.NDGWVPISTIAT

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FIG. 18

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1 aactcattta attactaatt taatcaacaa gattgataaa aagcagtaaa taaaacccaa
61 tagattttaat ttgaaagta tcaattgaaa aatggaaatt gaaaacaact aagcacaata
121 gccaaaagcc gaaaaattgt ggtgggaact tgaattagag atgcaagaaa accaaaatga
181 tatataagtt agggttaaga ttgacgatcc taagcaatat ctctgtaacg tcaactgcagc
241 atgtttgttg taggaaggta gttactacta agataaagat gaaagaagat atatcatcac
301 taaagcactt cttgaggttg ctgagtgctga tcttgagttc atctgctagt tggcagtcct
361 catccgtaat gaactttaca tcagaactac cactaactac attgtagcat tttgtgttgt
421 ccacaagaat actcaaccat tcctcgaaaa gtacttcaac aaagcagtac ttttgcctaa
481 tgacttactg gaagtctgtg aatttgcata ggttctctat atttttgatg caactgaatt
541 caaaaatttg tatcttgata ggatactttc ataagatatt cgtaaggaac tcactttccg
601 taagtgttta caaagatgcg tcagaagcaa gttttctgaa ttcaacgaat actaacttgg
661 taagtattgc actgaatcct aacgtaagaa aacaatgttc cgttacctct cagttaccaa
721 caagtaaaag tgggattaaa ctaagaagaa gagaaaagag aatctcttaa ccaaacttta
781 ggcaataaag gaattctgaag ataagtccaa gagagaaaact ggagacataa tgaacgttga
841 agatgcaatc aaggctttta aaccagcagt tatgaagaaa atagccaaga gatagaatgc
901 catgaagaaa cacatgaagg cacctaaaat tcctaactct accttggaat caaagtactt
961 gaccttcaag gatctcatta agttctgcca tatttctgag cctaaagaaa gagtctataa
1021 gatccttggt aaaaaatacc ctaagaccga agaggaatac aaagcagcct ttggtgatct
1081 tgcattctgca ccttcaatc ctgaattggc tggaaagcgt atgaagattg aaatctctaa
1141 aacatgggaa aatgaactca gtgcaaaagg caacactgct gaggtttggg ataattttaat
1201 ttcaagcaat taactcccat atatggccat gttacgtaac ttgtctaaca tcttaaaagc
1261 cgggtgttca gatactacac actctattgt gatcaacaag atttgtgagc ccaaggccgt
1321 tgagaactcc aagatgttcc ctcttcaatt ctttagtgcc attgaagctg ttaatgaagc
1381 agttactaag ggattcaagg ccaagaagag agaaaaatat aatcttaaaag gtcaaatcga
1441 agcagtaaaag gaagttgttg aaaaaaccga tgaagagaag aaagatatgg agttggagta
1501 aaccgaagaa ggagaatttg ttaaagtcaa cgaaggaatt ggcaagcaat acattaactc
1561 cattgaactt gcaatcaaga tagcagttaa caagaattta gatgaaatca aaggacacac
1621 tgcaatcttc tctgatgttt ctggttctat gagtacctca atgtcaggtg gagccaagaa
1681 gtatggttcc gttcgtaact gtctcgagtg tgcattagtc cttggtttga tggtaaaata
1741 acgttgtgaa aagtcctcat tctacatctt cagttcacct agttctcaat gcaataagtg
1801 ttacttagaa gttgatctcc ctggagacga actccgctct tctatgtaaa aacttttgca
1861 agagaaagga aaacttggtg gtggtactga tttcccctat gagtgcattg atgaatggac
1921 aaagaataaaa actcacgtag acaatatcgt tattttgtct gatatgatga ttgcagaagg
1981 atattcagat atcaatgtta gaggcagttc cattgttaac agcatcaaaa agtacaagga
2041 tgaagtaaat cctaacatta aaatctttgc agttgactta gaaggttacg gaaagtgccct
2101 taatctagggt gatgagttca atgaaaacaa ctacatcaag atattcggta tgagcgattc
2161 aatcttaaaag ttcatctcag ccaagcaagg aggagcaaat atggtcgaag ttatcaaaaa
2221 ctttgccctt caaaaaatag gacaaaagtg agtttcttga gattcttcta taacaaaaat
2281 ctcacccac tttttgtttt tattgcatga ccattatgaa atttaaatat ttatctattt
2341 atttaagtta cttacatagt ttatgtatcg cagtctatta gcctattcaa atgattctgc
2401 aaagaacaaa aaagattaaa a

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FIG. 19

FIG. 17

FIG. 17

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MEIENNAQAPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL
VNVTAACLLQEGSYQDKDERRYIITKALLEVAESDPEFICQLA
VYIRNELYIRTTTNYIVAFVHKNTPPFIEKYFNKAVLLPNDL
LEVCEFAQVLYIFDATEFNKLYLDRILSQDIRKELTFRKCLQRC
VRSKFSEFNEYQLGKYCTESQRKKTMFYRLSVTNKQKWDQTKKK
RKENLLTKLQAIKESDKSKRETGDIMNVEDAIKALPAVMKKI
AKRQNAKMKHMKAPKIPNSTLESKYLTFKDLIKFCHISEPKERV
YKILGKKYPKTEEEYKAAFSDASAPFNPELAGKRMKIEISKW
ENELSAKGNATAEVDNLISSNQLPYMAMLRNLSNILKAGVSDTT
HSIVINKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKR
ENMNLKGQIEAVKEVVEKTDEEKKDMELEQTEEGEFVKVNEGIG
KQYINSIELAKIAVNKNLDEIKGHTAIFSDVSGSMSTSMSSGA
KKYGSVRTCLECALVGLMVQRCCKSSFYIFSSPSSQCNKCYL
EVDLPGEDELPSMQKLLQEKGLGGGTDFPYECIDEWTKNKTTHV
DNIVILSDMMIAEGYSIDINVRGSSIVNSIKKYKDEVNPNIKIFA
VDLEGYGKCLNLGDEFNENNYIKIFGMSDSLKFIKQGGANM
VEVIKNFALQKIGQK

FIG. 20

MSRRNQKKPQAPIGNETNLDFVLQNLVYKSQIEHYKTQQQIK
EEDLKLKFKNQDQDGNNGNDDEENNSNKQQLLRNVNQIKQ
QVQLIKKVGSKVEKDLNLDENKKNGLSEQQVKEEQLRITITEE
QVKYQNLVFNMDYQDLNLSGGHRRHRRETQDTEKWEFISHDQ
KNYVSIYANQKTSYCWWLKDYFNKNYDHLNVNINRLETEAEFY
AFDDFSQTIKLTNNSYQTVNIDVNFDMNLCILALLRFLSLERF
NILNIRSSYTRNQYNFEKIGELLETFIAVVFSHRHLQGIHLQVP
CEAFQYLVNSSSQISVKDSQLQVYSFSTDCLKLVDTNKVQDYFKF
LQEFPRLTHVSQQAIPVSATNAVENLNVLLKKVKHANLNLVSI
TQFNDFYFVNLOHLKLEFGLNLTQKLENLLSISQSKNL
KFLRLNFYTYVAQETSRLQILQATTIKNLKNKNQEETPETKD
ETPSESTSGMKFFDHLSELTELEDFSVNLQATQEIYDSLHKLII
RSTNLKKFKLSYKYEMEKSKMDTFIDLKNIYETLNNLKRCVNI
SNPHGNISYELTNKDSTFYKFKLTNLQELQHAKYTFKQNEFQFN
NVKSAKIESSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPN
NIQKNPFKNPPLLFFKQFEQLKNLENVSINCLDQHILNSISEF
LEKNKKIKAFILKRYLLQYLDYTKLFTLQQLPELNQVYINQ
QLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSTLQLIDFD
QNTVSDDSIKKILESISESKYHHYLRNLPSQSSSLIKSENEEIQ
ELLKACDEKGVLVKAYYKFLCLPTGYDYDYNDRW

FIG. 22

MKILFEFIQDKLDIDLQTNSTYKENLKCGLHFNGLDEILTTCFAL
PNSRKIALPCLPGDLSHKAVIDHCIIYLLTGELYNNVLTFGYKI
ARNEDVNNSLFCFSANVNTLLKGAAMKMFHSLVGTAFVDDLII
NYTVIQFNGQFFTQIVGNRCNEPHLPPKWVQRSSSSSATAAQIK
QLTEPVTNKQFLHKLINSSSFFPYSKILPSSSSSIKKLTDLREA
IFPTNLVKIPQRLKVRINLTQKLLKRHKRLNYSILNSICPPL
EGTVLDLSHLSRQSPKERVLFIIIVILQKLLPQEMFGSKKNKGK
IIKNLNLNLLSLPLNGYLPFDLKLKRLKDFRWLFISDIWFTKH
NFENLNQLAICFISWLFRLIPKIIQTFFYCTEISSTVTIVYFR
HDTWNKLIPTFIVEYFKTYLVENNVCRNHNSYTLNFNHNSKMRI
IPKKSNNEFRIIAIPCRGADEEEFTIYKENHKNAIQPTQKILEY
LRNKRPTSFTKIYSPTQIADRIKEFKQRLKKFNNVLPPELYFMK
FDVKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFNTNTGVL
KLFNVVNASRVKPYELYIDNVRTVHLSNQDVINVVEMEIFKTA
LWVEDKCYIREDGLFQGSLSAPIVDLVYDDLLEFYSEFKASPS
QDTLILKLADDFLIISTDQQQVINIKKLAMGGFQKYNANANRDK
ILAVSSQSDDDTVIQFCAMHIFVKELEVWKHSSTMNHFHRSKS
SKGIFRSLIALFNTRISYKTIDTNLSTNTVLMQIDHVVKNISE
CYKSAFKDLSINVTQNMQFHSFLQRIIEMTVSGCPITKCDPLIE
YEVRFITLNGFLESLSNNTSKFKDNIIILRKEIQHLQAYIYIYI
HIVN

FIG. 23

0076622 002004

1 tcaatactat taattaataa ataaaaaaaa gcaaactaca aagaaaatgt caaggcgtaa
 61 ctaaaaaaag ccataggctc ctataggcaa tgaacaaaat cttgattttg tattacaaaa
 121 tctagaagtt tacaaaagcc agattgagca ttataagacc tagtagtaat agatcaaaaga
 181 ggaggatctc aagcttttaa agttcaaaaa ttaagattag gatggaaact ctggcaacga
 241 tgatgatgat gaagaaaaca actcaaaataa ataataagaa ttattaagga gagtcaatta
 301 gattaagtag caagtttaat tgataaaaaa agttggttct aaggtagaga aagatttgaa
 361 tttgaacgaa gatgaaaaca aaaagaatgg actttctgaa tagcaagtga aagaagagta
 421 attaagaacg attactgaag aatagggttaa gtattaaaaat ttagtattta acatggacta
 481 ccagtttagat ttaaattgaga gtggtggcca tagaagacac agaagagaaa cagattatga
 541 tactgaaaaa tggtttgaaa tatctcatga ccaaaaaaat tatgtatcaa tttacgccaa
 601 ctaaaagaca tcatattggtt ggtggcttaa agattatttt aataaaaaa attatgatca
 661 tcttaattgta agcattaaca gactagaaac tgaagccgaa ttctatgcct ttgatgattt
 721 ttcacaaaaca atcaaaactta ctaataattc ttactagact gttaacatag acgttaattt
 781 tgataataat ctctgtatac tcgcattgct tagattttta ttatcactag aaagattcaa
 841 tatttttgaat ataagattctt cttatacaag aaattaatat aattttgaga aaattgggtga
 901 gctacttgaa actactcttcg cagttgtctt ttctcatcgc cacttacaag gcatttcattt
 961 acaagttcct tgcgaagcgt tctaataattt agttaactcc tcatcataaa ttagcggttaa
 1021 agatagctaa ttataggtat actctttctc tacagactta aaattagttg acactaacia
 1081 agtccaagat tatttttaagt tcttataaga attccctcgt ttgactcatg taagctagta
 1141 ggctatccca gttagtgcta ctaacgctgt agagaacctc aatgttttac ttaaaaaggt
 1201 caagcatgct aatcttaatt tagtttctat ccctacctaa ttcaattttg atttctactt
 1261 tgttaatttta taacatttga aattagagtt tggattagaa ccaaatattt tgacaaaaca
 1321 aaagcttgaa aatctacttt tgagtataaa ataatacaaaa aatcttaaat ttttaagatt
 1381 aaactttttac acctacgttg ctttaagaaac ctccagaaaa cagatattaa aacaagctac
 1441 aacaatcaaaa aatctcaaaa acaataaaaa tcaagaagaa actcctgaaa cttaaagatga
 1501 aactccaagc gaaagcacaa gtggtatgaa attttttgat catctttctg aattaaccga
 1561 gcttgaagat ttcagcgtaa acttgtaagc taccacagaa atttatgata gcttgacaaa
 1621 acttttgatt agatcaacaa atttaaagaa gttcaaatta agttacaaat atgaaatgga
 1681 aaagagtaaaa atggatacat tcatagatct taagaatatt tatgaaacct taaacaatct
 1741 taaaagatgc tctgttaata tatcaaatcc tcatggaac atttcttatg aactgacaaa
 1801 taaagattct actttttata aatttaagct gaccttaaac taagaattat aacacgctaa
 1861 gtatactttt aagtagaacg aatttttaatt taataacggt aaaagtgc aaattgaaatc
 1921 ttcttcatta gaaagcttag aagatatgta tagtctttgc aaatctattg cttcttgtaa
 1981 aaattttaca aatgttaata ttatcgccag tttgctctat cccaacaata tttagaaaaa
 2041 tccttttcaat aagcccaatc ttctattttt caagcaattt gaataattga aaaatttgga
 2101 aaatgtatct atcaactgta ttcttgatca gcatatactt aattctattt cagaattctt
 2161 agaaaagaat aaaaaaataa aagcattcat tttgaaaaga tattatttat tacaatatta
 2221 tcttgattat actaaattat ttaaaacact tcaatagtta cctgaattaa attaagttta
 2281 cattaattag caattagaag aattgactgt gagtgaagta cataagtaag tatgggaaaa
 2341 ccacaagcaa aaagctttct atgaaccatt atgtgagttt atcaaagaat catcctaacc
 2401 ccttttagcta atagattttg accaaaacac tgtaagtgat gactctatta aaaagatttt
 2461 agaactctata tctgagtcta agtatcatca ttatttgaga ttgaacccta gttaatctag
 2521 cagttttaatt aaatctgaaa acgaagaaat ttaagaactt ctcaaagctt gcgacgaaaa
 2581 aggtgtttta gtaaaagcat actataaatt cctctatgt ttaccaactg gtacttatta
 2641 cgattacaat tcagatagat ggtgattaat taaatattag tttaaataaa tattaaatat
 2701 tgaatatttc tttgcttatt atttgaataa tacatacaat agtcattttt agtgttttga
 2761 atatatttta gttattttaat tcattatttt aagtaataaa ttatttttca atcatttttt
 2821 aaaaaatcg

FIG. 21

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Oxytricha
Euplotes

LCVSYILSSFYANLEENALQFLRKESMDPEKPETNLLMRLT
LCVSSILSSFYATLEESSLGFLRDESMNPENPNVLLMRLT

FIG. 24

ATTTATACTCATGAAAATCTTATTTCGAGTTCATTCAAGACAAGCTTGACATTGATCTACA
GACCAACAGTACTTACAAAAGAAAATTTAAAATGTGGTCACCTTCAATGGCCTCGATGAAAT
TCTAACTACGTGTTTCGCACCTACCAAATTCAGAAAAATAGCATTACCATGCCTTCCTGG
TGACTTAAGCCACAAAGCAGTCATTGATCACTGCATCATTTACCTGTTGACGGGCGAATT
ATACAACAACGTACTAACATTTGGCTATAAAAATAGCTAGAAAATGAAGATGTCAACAATAG
TCTTTTTTGGCATTCTGCAAATGTTAACGTTACGTTACTGAAAGGCGCTGCTTGGAAAAAT
GTTCCACAGTTTGGTCGGTACATACGCATTCGTTGATTTATTGATCAATTATACAGTAAT
TCAATTTAATGGGCAGTTTTTCACTCAAATCGTGGGTAACAGATGTAACGAACCTCATCT
GCCGCCCAAATGGGTCCAACGATCATCCTCATCATCCGCAACTGCTGCGCAAATCAAACA
ACTTACAGAACCAGTGACAAATAAACAAATTTTACACAAGCTCAATATAAATTCCTCTTC
TTTTTTTTCCCTTATAGCAAGATCCTTCCTTCATCATCATCTATCAAAAAGCTAACTGACTT
GAGAGAAGCTATTTTTTCCCACAAATTTGGTTAAAAATTCCTCAGAGACTAAAGGTACGAAT
TAATTTGACGCTGCAAAAGCTATTAAAGAGACATAAGCGTTTGAATTACGTTTCTATTTT
GAATAGTATTTGCCACCATTGGAAGGGACCGTATTGGACTTGTGCGCATTTGAGTAGGCA
ATCACCAAAGGAACGAGTCTTGAAATTTATCATTGTTATTTTACAGAAGTTATTACCCCA
AGAAATGTTTGGCTCAAAGAAAAATAAAAGGAAAAATTTATCAAGAATCTAAATCTTTTATT
AAGTTTACCCTTAAATGGCTATTTACCATTGTATAGTTTGTGAAAAAGTTAAGATTAAA
GGATTTTCGGTGGTTGTTTCATTTCTGATATTTGGTTACCAAGCACAAATTTTGAAAACTT
GAATCAATTTGGCGATTTGTTTTCATTTCCCTGGCTATTTAGACAACCTAATTTCCCAAAATAT
ACAGACTTTTTTTTACTGCAACCGAAATATCTTCTACAGTGACAATTTGTTTACTTTAGACA
TGATACTTTGGAATAAACTTATCACCCTTTTATCGTAGAATATTTTAAAGACGTACTTAGT
CGAAAACAACGTATGTAGAAACCATAATAGTTACACGTTGTCCAATTTCAATCATAGCAA
AATGAGGATTATACCAAAAAAAGTAATAATGAGTTTCAGGATTTATGCCATCCCATGCAG
AGGGGCAGACGAAGAAGAAATTCACAAATTTATAAGGAGAATCACAAAAATGCTATCCAGCC
CACTCAAAAAATTTTAGAATACCTTAAGAAAAACAAAAGGCCGACTAGTTTTTACTAAAAATATA
TTCTCCAACGCAAATAGCTGACCGTATCAAAGAATTTAAGCAGAGACTTTTAAAGAAAT
TAATAATGTCTTACCAGAGCTTTATTTTCATGAAATTTGATGTCAAATCTTGCTATGATTC
CATACCAAGGATGGAATGTATGAGGATACTCAAGGATGCGCTAAAAAATGAAAAATGGGTT
TTTCGTTAGATCTCAATATTTCTTCAATACCAATACAGGTGTATTGAAGTTATTTAATGT
TGTTAACGCTAGCAGAGTACCAAAACCTTATGAGCTATACATAGATAATGTGAGGACGGT
TCATTTTATCAAATCAGGATGTTATAAACGTTGTAGAGATGGAAATATTTAAAACAGCTTT
GTGGGTTGAAGATAAGTGTACATTAGAGAAGATGGTCTTTTTTCAGGGCTCTAGTTTATC
TGCTCCGATCGTTGATTTGGTGTATGACGATCTTCTGGAGTTTATAGCGAGTTTAAAGC
CAGTCCTAGCCAGGACACATTAATTTTAAACCTGGCTGACGATTTCTTTATAATATCAAC
AGACCAACAGCAAGTGATCAATATCAAAAAGCTTGCCATGGGCGGATTTCAAAAAATATAA
TGCGAAAGCCAATAGAGACAAAATTTTAGCCGTAAGCTCCCAATCAGATGATGATACGGT
TATTCAATTTTGTGCAATGCACATATTTGTTAAAGAATTTGGAAGTTTGGAACATTCAG
CACAATGAATAATTTCCATATCCGTTTCGAAATCTAGTAAAGGATATTTTCGAAGTTTAAAT
AGCGCTGTTTAAACACTAGAATCTCTTATAAAAACAATTGACACAAATTTAAATTTCAACAAA
CACCGTTCTCATGCAAATTGATCATGTTGTAAAGAACATTTCCGAATGTTATAAAATCTGC
TTTTAAGGATCTATCAATTAATGTTACGCAAAATATGCAATTTTCATTCGTTCTTACACG
CATCATTTGAAATGACAGTCAGCGGTTGTCCAATTTACGAAATGTGATCCTTTAATCGAGTA
TGAGGTACGATTACCATATTTGAATGGATTTTGGAAAGCCTATCTTCAACACATCAAA
ATTTAAAGATAATATCATTTCTTTTGAGAAAGGAAATTCACACTTGCAAGC

FIG. 26

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human	Motif 0	
tez1		AKFLHMLMSVYVVELLRSPFYVVTETTFQKNR
EST2		ISLEWLVLGKRSNAKMCLSDFEKKQIFAEFIYMLNFIIPILQSPFYITESSDLNR
p123		LKDFRWLFISD---IWFTKHNFENLQLAICFISWLFQLPKIIQITFFYCTEISSVT- TREISWMQVET-SAKHFIYFDHEN-IYVLWKLRLWIFEDLVSLIRCFFYVTEQQKSYSK * * * *
human	Motif 1	
tez1		LFFYKSWSKLQSIGTRQHLKRVQLRDVSEAEVRQHRARPALLTSRLRFIPKP--DGL
EST2		TVYFRKDIWKLLCRPFI-TSMKMEAFKINENNVRMDTQK-TTLPPAVIRLLPKK--NTF
p123		IVYFRHDTWNLITFFIVEYFKTYLVENNVCRNHNSYTLS--NFNHSKMRIIPKKSNEF TYYYRKNIWDVIMKMSI-ADLKKETLAEVQKEVEEMKKS-LGFAPGKLRLLIPKK--TTF * * * *
human	Motif 2	
tez1		RPIVNM DYVVGARTFREKRAERLTSRVKALF-SVLNYERA
EST2		RLITN-LRKRFLIKGSKNKKMLVSTNQTLRPVASILKHLNEESSGIPFNLEVMKLLTF
p123		RIIAIPCRGADEEEFTYKENHKNAIQPTQKILEYLRNKRPTSTFKIYSPTQIADRIKEF RPIMTFNKKIVNSDRKTTKLTNTKLLNSHMLMLTKLN-RMFKDPFGFAVFNVDVMMKY * * * *
human	Motif 3 (A)	
tez1		KKDLLKHRMFGR-KKYFVRIDIKSCYDRIKQDLMFRIVKK-KLKDPEFVIRKYATIHATS
EST2		KQRLKKFN NVLP ELYFMKFDVKSCYDSTPRMECMRLLKD-ALKNENGFFVRSQYFFNTN
p123		EEFVCKWKQVGQPKLFFATMDIEKCYDSVNREKLS TFLKTTKLLSSDFWIMTAQILKRKN * * * *

FIG. 25

1. *Chlorophyll a* (Chl *a*) and *Chlorophyll b* (Chl *b*) were extracted from 0.5 g of fresh leaves using 10 mL of 80% methanol. The extracts were centrifuged at 1000g for 5 min and the supernatant was transferred to a vial. The process was repeated until all the leaves were extracted. The supernatants were then combined and the solvent was evaporated under reduced pressure. The residue was dissolved in 1 mL of 80% methanol and the solution was filtered through a 0.22 µm filter. The filtrate was then analyzed by HPLC.

FIG. 28

FIG. 29

ggtaccgatttacttcttcttataagtaattggttcttctctcgaaagctctctaaatctctgaaatatttttacaaga
actcaataaacaataccaagtcaaatccaatataagtggttattagtgatgataaatttctattttatcggtcggtta
ccaagtataaggacaaaagaacaacttcttccccctaaagacttttactatttatttatttcaaatataatttctg
ggttcgcttacttttaactcggtactgttttagtctactcttagccaacgcgtgtttctaccccgctaatggatatt
agctcttggaagtacacagaaatccttacaactctctgtagactataatagattcattacagtcggtcgcatactc
ttaacatggagccttacacttttagatgagtcacgtcgatgatggagtatttggtatcatccaaagtttgccttgaaaag
gttgataaattatttgcaaaatcgtccttagtggttaacgcgaaagttttttctgctgacacgcgtctagcatg
attgagataattcaaaaaatttctatccactacaactcctttaaagcggttttatttttctatttctattcctcatgtgtt
ccaatatgtatcgtattaggttcttccgttttactcctggaaatcgtaaccttttctactattcccccataatga
ataactaaaattagtttcgcttataattagatagtagaagaattggtgattctactcgtgtaagtatttagtttaaa
gatactttgcaaaacatttattagctatcattataaaaaaaacctcattataataattataatcaattttgcggtc
actatttttaaaaacgttatgatcagtaggacactttgcataataatagttatgcttaagtgttacttgaacttgcat
GACCGAACACATACCCCAAGAGGATTCCTCGCTTTAGAGAAATATATGATATACCTATGTTACCTTAAATGATT
ATGTAACAACCTTTTGGAGAGGTCGCGCAAGCTCTGTATAGCAATATATGCGAACGCTTGAGAGCGATGTACAAACG
TCCTTTCTATTTCATTCGACTGTAGTCGGCTTCGACAGTAAGCCAGATGAAGGTGTTCAATTTCTCTCCAAA
ATGCTCACAGTCAGAGgtatataattttgttttggatttttctatctcggaatagctaaatataatgggcagCTAATAGC
GAATGTTGTAACACAGATGTTGATGAAAGTTTGGAGCTCGAAGGAATCTACTGATGAAGGGTTTCCATGtgaaggt
attcctaattgtgaaaataattacctgcaattactgtttcaaaagagattgtatttaacccaataaagAACATCATGAAGATTTC
GAGCATGTCATGTAAACGGAGTACAAAATGATCTCGTTTCTACTTTCTCTAATTAACCTTATATCTACTTGAAGTCAAAA
AATTGGCAACTTTTGTAGAAATgtataatccggttaagattgttgcgcacttttgacaagactgacaagataagTATCGG
CAGTGATGCCATGCTACTTATTATCCAAAGGAAGTTTGGAGCTCTTCCAAATGACAAATTCCTTCAGATTTCG
GCATACCACCTTTTAAATAATGTGTTTGGAGAACTGTGTCAAAAAGAAAGAACCCATTTGAAACATCCCATTACT
CAAAATAAAGCGCCCAAGAGTTTCTGGAATAGCATTTCAATAGTGTGTTTACAGGTTTACAGGTCATCTCTA
TAAGAAGTTTAAAGCAAGtaactaatactgttactctcataactaaatttttagATCTATATTTTAACTTACACTCTATT
GTGATCGGAACACAGTACATGTGGCTTCAATGGATTTCAGGCAATTTGGACTTTATAACGCATTTCAAGTGAAG
CAATTGCACAAAGTATCCACTGTGTATCACAGAGTACAGTTGTGCCCAACGCTCTCCTAAAGGTATACCCTTTAAATGA
ACAAACAGCAAGCGACTCCATCGTATTCTCTATCAAAAGTTTACAACCAATATTGCCCCATATTATGACCCACGATG
ATGAAAAAATCCTTAGTTATTCCTTAAAGCCGAACCCAGGTGTTGCGTTTCTTCGATCCCATCTTGTTCGAGTGTTCCT
AAATTAATCTGGGTAAACCAAGGATATTGAGATAATATAAAGgtattgtataaaatttattaccactaacgatttc
accagACCTCGAAACTTTCTTGAATTAATCGAGATACGAGTCTTTTAGTTTACATTAATTAATGAGTAACATAAAGgtaa
tatgcgaattttttaccattaaataacaaatcagATTTTCAGAAATGAAATGAAATCGAACTGTTTATTATTAGAAAGATATTT
AAATGTGCTTAAGTGATTTTGAGAAACGCAAGCAAAATATTTCGGAAATTCATCTACTGCTATACAAATTCGTTTATAAT
ACCTATTTTTACAATCTTTTATTATCACTGAATCAAGTATTGAAATCGAAATGAACTGTTTATTATTAGAAAGATATTT
GGAAACTCTTGTGCCGACCTTTTATACATCAATGAATGAAAGCGTTTGAAGAAATTAACGAGgtatttttaaggtatt
ttttgcgaagaagctaaatattttcagaACAAATGTTAGGATGATCTCAGAAACACTACTTTGCTCCAGCAGTATTTCGTC
TATTACCTAAGAAAGATACCTTTCCTCATTTACGAATTAAGAAAAAGATTTCTTAATAAAGgtattaaatttttggtoat
caatgtactttacttctaatctatttagcagatGGGTCAACAAAAAATGTTAGTCAGTACGACCAAACTTTACG
ACCTGTGGCATCGATACTGAACACATTTAATCAATGAAGAAAGTAGTGGTATTCCATTTTAACTTGGAGGTTTACATGAAGC

FIG. 30

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FIG. 30
(CONTINUED)

(CONTINUED)

EST2 pep	FFYCTEISST	VTIVYFRHDT	WN----	KLIT	P-----	FIVE	YFK-TYLVEN	40
Euplotes pep	FFYVTEQOKS	YSKTYYYRKN	IMDWI-MKMS	IAD----	LKK	ETLA--	EVQE	43
Trans of tetrahymen	-----KHKE	GSQIFYVRKP	IWKLVSKLTI	VKVRIQFSEK	NKQMKNNFYQ			44
Consensus	FFY.TE..K.	S..YYRK.	IW....-KL..-F..KV..			50
EST2 pep	NVCRNHSY-	-----	TLSNFNHSM	RIIPKKNNE	FRITAI	PCRG		79
Euplotes pep	KEVEWKKS	-----	---GFAPCKG	RIIPKKNNE	FRITAI	PCRG		78
Trans of tetrahymen	KIQLEENLE	KVEEKLIPED	SFQYPOGKL	RIIPKKS--	FRITMTFLRK			92
Consensus	K...E.....	-----F..GKL	RIIPKKNNE	FRITMTFLRK			100
EST2 pep	ADEEFTIYK	ENHKNAIQPT	QKILEYTRNK	RPTSFTKIYS	PTQIADRIKE			129
Euplotes pep	IVNSDRKTK	LTNTTKLNS	HMLKTLKN-	-----RMFK	-DPFGFAVN			120
Trans of tetrahymen	DKQKNIK---	LNLNQILMDS	QLVFRNLKD-	-----ML-G	-QKIGYSVFD			130
ConsensusK..K	LN.N..L..S	QL.L..LKN-	-----	..IG..VF.			150
EST2 pep	FKQRLKKN	NVL-----	RIIPKKNNE	FRITAI	PCRG			157
Euplotes pep	YD-DVMKKYE	EFVCKWKQVH	CPKLIFFATMD	IEKCYD				155
Trans of tetrahymen	NK-QISEKFA	QFIEKWKNG	RPCLVYVTL-	-----				158
Consensus	.K....KFF.	F..KWK..G	RIIPKKNNE	FRITAI	PCRG			186

FIG. 31

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S-1: FFY VTE TTF QKN RLF FYR KSV WSK
 S-2: RQH LKR VQL RDV SEA EVR QHR EA
 S-3: ART FRR EKR AER LTS RVK ALF SVL NYE

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q
 A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS
 A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV

FIG. 32

Poly 4

5'- t a a g c c t c g
 cag acc aaa gga att cca taa gg -3'
 Q T K G I P Q G

4(B')

5(c')

D D Y L L I T
 3'- ctg ctg atg gag gag tag tgg -5'
 a a a a a a a a
 t t t t
 c c
Poly 1

FIG. 34

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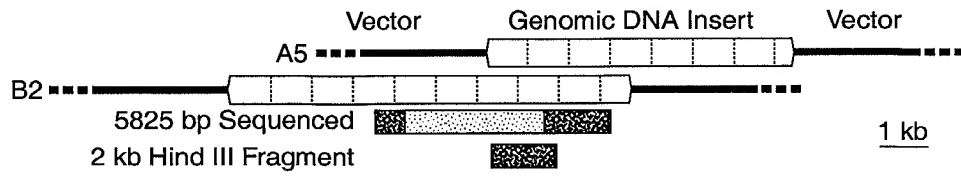


FIG. 33A

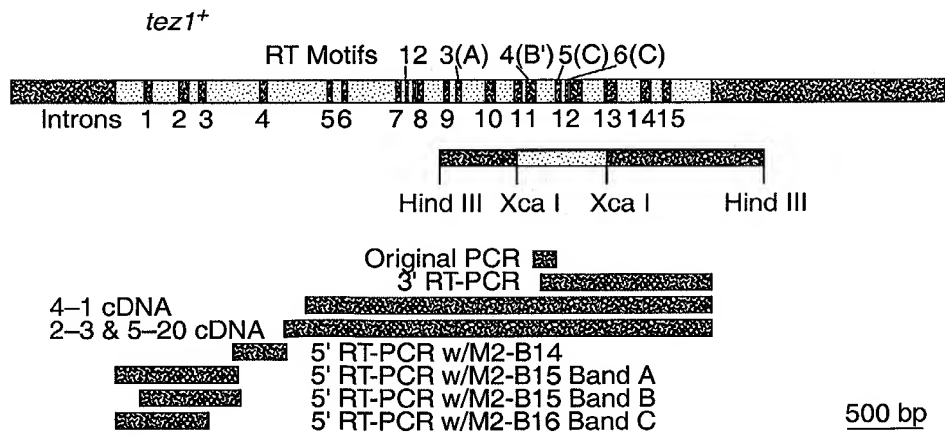


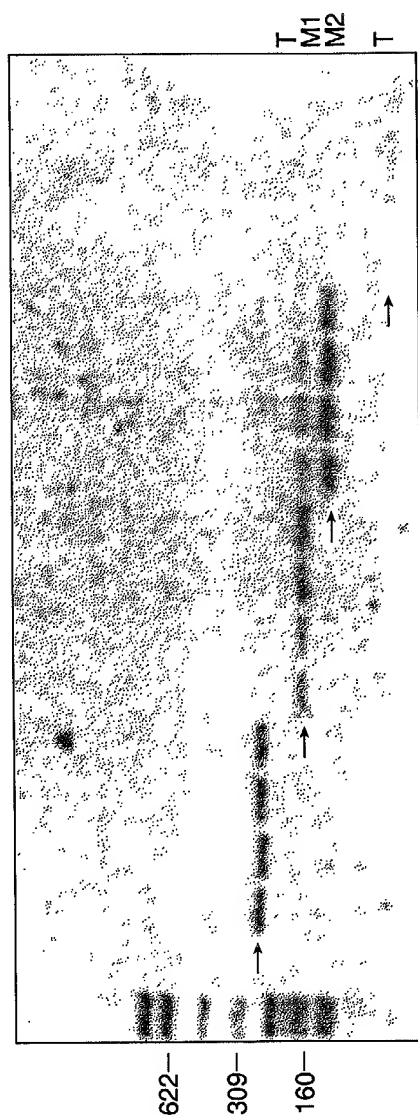
FIG. 33B

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Motif C (5)
DDYLLIT

Motif B' (4)
QTKGIPQG

FIG. 35

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Ot LCVSYILSSFYANLEENALQFLRKESMDPEKPETNLLMRLT
 Ea_p123 KGIPOGLCVSSILSSFYATLEESSLGFLRDESMNPENVNLLMRLTDDYLLIT
 Sp_M2 SILSSFLCHFYMEDLIDEYLSFTKKK-----GSVLLRVV
 Sc_p103 DGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS-----QDTLLILKLADDFLIIS
 * . . *

Q K V G I P Q G <---Actual Genomic Sequence.
 caa aaa ggt ggt atc cct cag gg.....

Poly 4 t t c
 t a a g c c t c g
 cag acc aaa gga att cca taa gg ---->

ag acc aaa gga att cca tca ggc tca att ctg tca tct ttg tgt cat ttc tat atg
 tc tgg ttt cct taa ggt agt ccg agt taa gac agt aga aaa aac aca gta aag ata tac

K G I P S G S I L S S F L C H F Y M

FIG. 36

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GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA
 CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC CCT AGT CAC AAC AAT GCT
 E D L I D E Y L S F T K K G S V L L R

GTA GTC gac gac tac ctc ctc atc acc
 CAT CAG ctg ctg atg gag gag tag tgg

V V D D Y L L I T

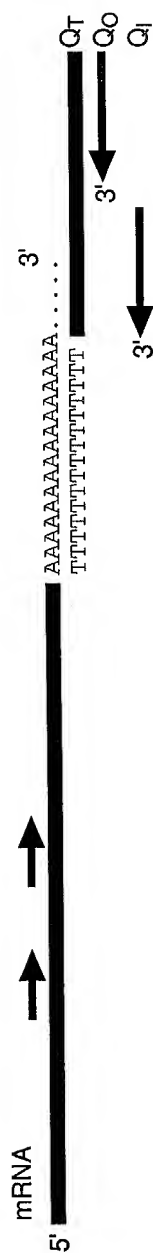
<----- ctg ctg atg gag gag tag tgg
 a a a a a a a
 t t t t t
 C C
Poly 1

.....gac gat ttc ctc ttt ata aca..... <---Actual Genomic Sequence
 D D F L F I T

FIG. 36
 (CONTINUED)

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1. Synthesis of cDNA with Q_T Primer



2. First Round PCR Using Outside Primer and Q₀ Primer



3. Second Round PCR Using Inside Primer and Q₁ Primer



4. Sequence Second Round PCR Products Using Inside Primer Q₁ Primer

FIG. 37

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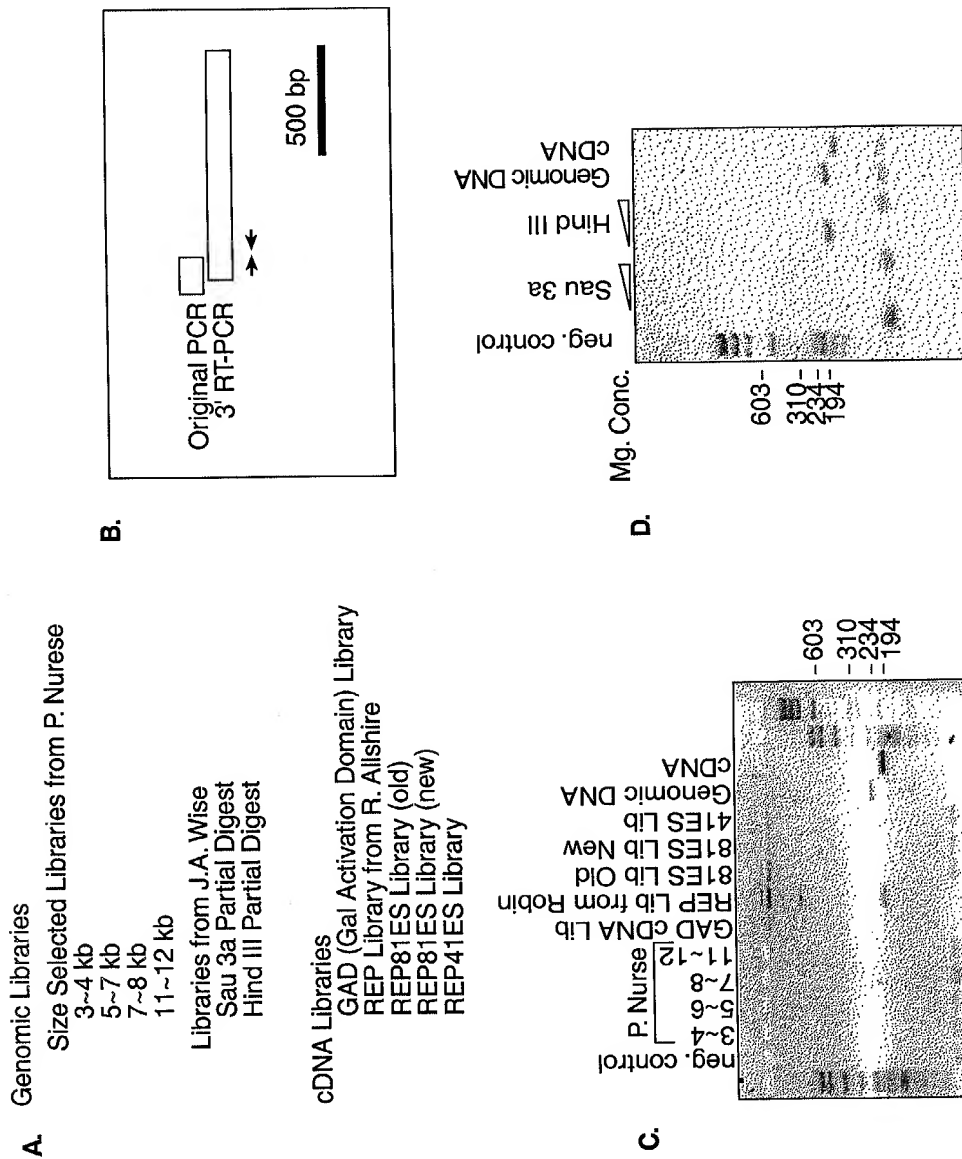


FIG. 38

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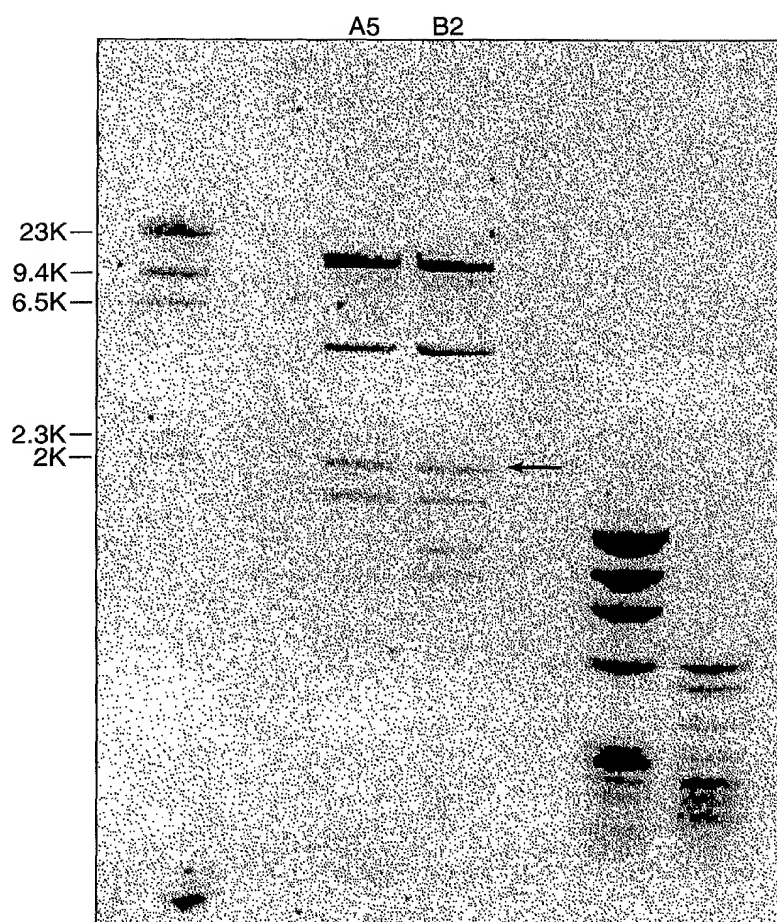


FIG. 39

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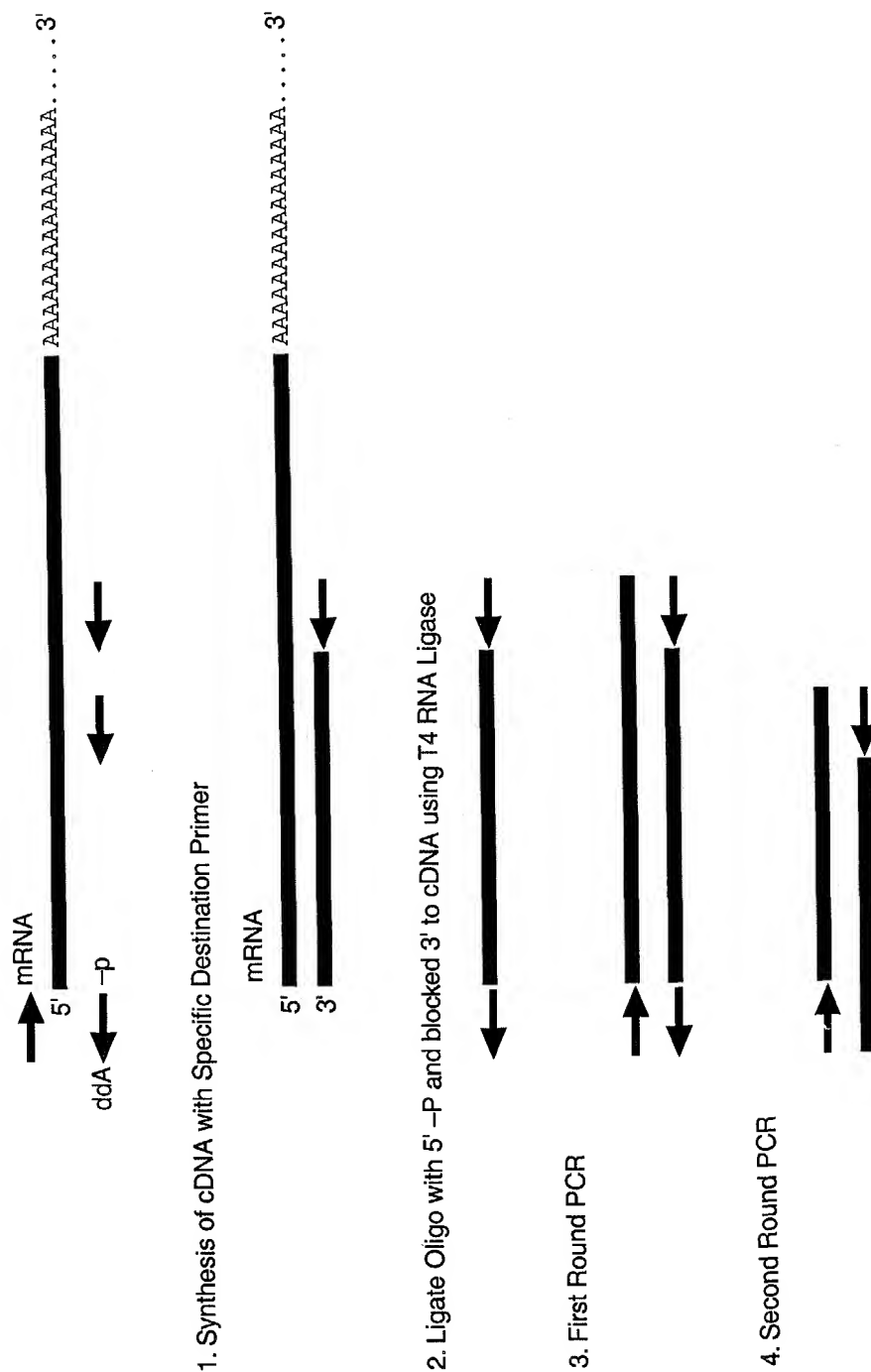


FIG. 40

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		Motif O	
S.p. Tez1p	(429) .	WLYNSFIIPILQSFYITESSDLRNRVTVPKDIW	... (35) ...
S.c. Est2p	(366) .	WLFRLPKIIQTFYCTEISSTVT-IVYFRHDTW	... (35) ...
E.a. p123	(441) .	WIFEDLVSLIRCFYVTEQQKSYKTYYYRKNIW	... (35) ...
		*** ** *	*
		Motif 1	K
		p hh h K	hR h
S.p. Tez1p		AVIRLLPKK--NTFRLITN-LRKRF	... (61) ...
S.c. Est2p		SKMRIIPKKSNNFRIIAPCRGAD	... (62) ...
E.a. p123		GKLRLLPKK--TTFRPIMTFNKKIV	... (61) ...
		*** ** *	*
		Motif 3 (A) AF	
		h hDh GY h	
S.p. Tez1p		KKYFVRIDIKSCYDRIKQDLMFRIVK	... (89) ...
S.c. Est2p		ELYFMKFDVKSCYDSIPRMECMRIK	... (75) ...
E.a. p123		KLFFATMDIEKCYDSVNREKLSTFLK	... (107) ...
		* * * ***	*
		Motif 4 (B')	
		hPQG pP hh h	
S.p. Tez1p		YLQKVGIPQGSILSSFLCHFYMEDLIDEYLSF	... (6) ...
S.c. Est2p		YIREDGLFQGSLSAPIVDLVYDDLLEFYSEF	... (8) ...
E.a. p123		YKQTKGIPQGLCVSSILSSFYATLEESSLGF	... (14) ...
		* * * ** *	*
		Y Motif 5 (C)	Motif 6 (D)
		h F DDhhh	Gh h ck h
S.p. Tez1p		VLLRVVDDFLFITVNNKDAKFFNLRLRGFEKHNFTSLEKTVINFENS	... (205)
S.c. Est2p		LILKLADDFLIIISTDQQQVINIKKLAMGGFKYNKANRDKILAVSSQS	... (173)
E.a. p123		LIMRLTDDYLLITTTQENNAVLFIKLINVSRENGFKFNKKLQTSFPPLS	... (209)
		** * * *	*

FIG. 41

A.		
Sp_Tip1p	1	-----MTEHHTPKSRILRFLNQYVYLCT 24
Sc_Est2p	1	-----MKILFEF 7
Ea_p123	1	MEVDVDNQADNHGHSALKTCCEEIKEAKTLYSW 33
Sp_Tip1p	25	LN DYVQLVLRGSPASSYSNICERLRSDVQTSFS 57
Sc_Est2p	8	IQDKLDIDLQTN--STYK--ENLKCCHFNGLD 35
Ea_p123	34	IQKVIRCRNQSQ--SHYK--DLEDIKIFAQTN 61
Sp_Tip1p	58	IFLHSTVVGFDISKPDQGVQFSSPKCSQSSELIAN 90
Sc_Est2p	36	EILTTTCFALPNRSR-KIALPCPLPGDLSHKAVIDH 67
Ea_p123	62	I VATTIPRDYNEEDFKVIARKEVFSTGLMIELIDK 94
Sp_Tip1p	91	VVKQMFDESFERR--NLLMKGFESMNHEDFRAMH 122
Sc_Est2p	68	CI IYLLTGELYN--NVLLTFGYKIARNED-- 93
Ea_p123	95	CLVELLS SSVSDVSDRQKLQCFFGFQKGNQ-- 122
Sp_Tip1p	123	VNGVQNDLVSITFPN YLISILESKNWQLLLEIIG 155
Sc_Est2p	94	--VNNSLFCCHSANVNVTLLKGAAWKMFHSLVVG 123
Ea_p123	123	--LAKTHLLTALSTQKQYFFQDEWNQVRAMIG 152
Sp_Tip1p	156	SDAMHYLLSKGSIFFEALPNDNYLQISGIPLEFKN 188
Sc_Est2p	124	TYAFVDLLIN YTVIQFN-GQFFTQIVGNRCNEP 155
Ea_p123	153	NELFRHLYTKYLI FQRTSEGTLVQFCGNNVFDH 185
Sp_Tip1p	189	NVFEETVSKKRKRRTIETSI TQN--KSARKEVS 218
Sc_Est2p	156	HLPPKWWQ--RSSSSSATAAQI--KQLTEPVT 183
Ea_p123	186	LKVNDKFDK-KQKGGAA DMNEPRCCSTCKYNVK 217

FIG. 42

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A.

Sp_Tip1p	219	W	N	S	I	S	I	S	R	F	S	I	F	Y	R	S	S	Y	K	K	F	K	Q	D	L	Y	F	N	L	H	S	I	C	D	251
Sc_Est2p	184	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	Q	F	L	H	K	L	N	I	N	S	S	S	F	F	P	200
Ea_p123	218	N	E	K	-	-	D	H	F	L	N	I	N	V	P	N	W	N	N	M	K	S	R	T	R	I	F	Y	C	T	H	F	N	248	
Sp_Tip1p	252	R	N	T	V	H	M	W	L	Q	W	I	F	P	R	Q	F	G	L	I	N	A	F	Q	V	K	Q	L	H	K	V	I	P	L	284
Sc_Est2p	201	-	-	-	-	-	-	-	-	Y	S	K	I	L	P	S	S	-	-	S	I	K	K	L	T	D	L	R	E	A	I	F	P	223	
Ea_p123	249	R	-	-	-	-	-	-	-	N	N	Q	F	F	K	H	E	F	V	S	N	K	N	I	S	A	M	D	R	A	Q	T	I	275	
Sp_Tip1p	285	V	S	-	-	-	Q	S	T	V	V	P	K	R	L	L	K	V	Y	P	L	I	E	Q	T	A	K	R	L	H	R	I	S	313	
Sc_Est2p	224	T	N	-	-	-	L	V	K	I	P	Q	R	L	K	V	R	I	N	L	T	L	Q	K	L	L	K	R	H	K	R	L	N	252	
Ea_p123	276	F	T	N	I	F	R	F	N	R	I	R	K	K	L	K	D	K	V	I	E	K	I	A	Y	M	L	E	K	V	K	D	F	N	308
Sp_Tip1p	314	L	S	K	V	N	N	H	Y	C	P	Y	I	D	-	T	H	D	D	E	K	I	L	S	Y	S	L	K	P	N	Q	-	-	-	342
Sc_Est2p	253	Y	V	S	I	L	N	S	I	C	P	P	L	E	G	I	V	L	D	L	S	H	L	S	R	Q	S	P	K	E	R	-	-	-	282
Ea_p123	309	F	N	Y	Y	L	T	K	S	C	P	L	P	E	N	W	R	E	R	K	Q	K	I	E	N	L	I	N	K	T	R	E	E	K	341
Sp_Tip1p	343	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	V	F	A	F	L	R	S	I	L	V	R	V	F	P	K	L	I	359	
Sc_Est2p	283	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	V	L	K	F	I	I	V	I	L	Q	K	L	P	Q	E	M	299	
Ea_p123	342	S	K	Y	E	E	L	F	S	Y	T	T	D	N	K	C	V	T	Q	F	I	N	E	F	F	Y	N	I	L	P	K	D	F	374	
Sp_Tip1p	360	W	G	N	Q	R	I	F	E	I	I	L	K	D	L	E	T	F	L	K	L	S	R	Y	E	S	F	S	L	H	Y	L	M	S	392
Sc_Est2p	300	F	G	S	K	N	K	G	K	I	I	K	N	L	N	L	L	L	S	L	P	L	N	G	Y	L	P	F	D	S	L	L	K	332	
Ea_p123	375	L	T	G	-	R	N	R	K	N	F	Q	K	V	K	K	Y	V	E	L	N	K	H	E	L	I	H	K	N	L	L	L	E	406	
Sp_Tip1p	393	N	I	K	I	S	E	I	E	W	L	V	L	G	K	R	S	N	A	K	M	C	L	S	D	F	E	K	R	K	Q	I	F	A	425
Sc_Est2p	333	K	L	R	L	K	D	F	R	W	L	F	I	S	-	-	D	I	W	F	T	K	H	N	F	E	N	L	N	Q	L	A	I	362	
Ea_p123	407	K	I	N	T	R	E	I	S	M	M	Q	V	E	T	S	-	A	K	H	F	Y	Y	F	D	H	E	N	-	I	Y	V	L	W	4

FIG. 42
(CONTINUED)

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A.	Sp_Tip1p	426	E	F	I	Y	W	L	N	S	F	I	I	P	I	L	Q	S	F	F	Y	I	T	E	S	S	D	L	R	N	R	T	V	Y	458	
	Sc_Est2p	363	C	F	I	S	W	L	F	R	Q	L	I	P	K	I	I	Q	T	F	F	Y	C	T	E	I	S	S	T	V	T	-	I	V	Y	394
	Ea_p123	438	K	L	L	R	W	I	F	E	D	L	V	V	S	L	I	R	C	F	F	Y	V	T	E	Q	Q	K	S	Y	S	K	T	Y	Y	470
	Sp_Tip1p	459	F	R	K	D	I	W	K	L	C	R	P	F	I	T	S	M	K	M	E	A	F	E	K	I	N	E	N	N	V	R	M	D	491	
	Sc_Est2p	395	F	R	H	D	T	W	N	K	L	I	T	P	F	I	V	E	Y	F	K	T	Y	L	V	E	N	N	V	C	R	N	H	N	S	427
	Ea_p123	471	Y	R	K	N	I	W	D	V	I	M	K	M	S	I	A	D	L	K	K	E	T	L	A	E	V	Q	E	K	E	V	E	E	W	503
	Sp_Tip1p	492	T	Q	K	T	T	L	P	A	V	I	R	L	L	P	K	K	-	-	N	T	F	R	L	I	T	N	L	R	K	R	F	L	522	
	Sc_Est2p	428	Y	T	L	S	N	F	N	H	S	K	M	R	I	I	P	K	S	N	E	F	R	I	I	A	I	P	C	R	G	A	D	460		
	Ea_p123	504	K	K	S	L	G	F	A	P	G	K	L	R	L	I	P	K	K	-	-	T	T	F	R	P	I	M	T	F	N	K	K	I	V	534
	Sp_Tip1p	523	I	K	M	G	S	N	K	K	M	L	V	S	T	N	Q	T	L	R	P	V	A	S	I	L	K	H	L	I	N	E	-	-	552	
	Sc_Est2p	461	E	E	E	-	-	F	T	I	Y	K	E	N	H	K	N	A	I	Q	P	T	Q	K	I	L	E	Y	L	R	N	K	R	P	491	
	Ea_p123	535	N	S	D	-	-	R	K	T	T	K	L	T	T	N	T	K	L	N	S	H	L	M	L	K	T	L	K	N	R	-	M	F	564	
	Sp_Tip1p	553	E	S	S	G	I	P	F	N	L	E	V	Y	M	K	L	L	T	F	K	K	D	L	L	K	H	R	M	F	G	R	-	K	K	584
	Sc_Est2p	492	S	F	T	K	I	Y	S	P	T	Q	I	A	D	R	I	K	E	F	K	Q	R	L	L	K	K	F	N	N	V	L	P	E	L	524
	Ea_p123	565	K	D	P	F	G	F	A	V	F	N	Y	D	D	V	M	K	K	Y	E	E	F	V	C	K	W	K	Q	V	G	Q	P	K	L	597
	Sp_Tip1p	585	Y	F	V	R	I	D	I	K	S	C	Y	D	R	I	K	Q	D	L	M	F	R	I	V	K	K	K	L	K	D	P	E	-	F	616
	Sc_Est2p	525	Y	F	M	K	F	D	V	K	S	C	Y	D	S	I	P	R	M	E	C	M	R	I	L	K	D	A	L	K	N	E	N	G	F	557
	Ea_p123	598	F	F	A	T	M	D	I	E	K	C	Y	D	S	V	N	R	E	K	L	S	T	F	L	K	T	T	K	L	L	S	S	D	F	630
	Sp_Tip1p	617	V	I	R	K	Y	A	T	I	H	A	T	S	D	R	A	T	K	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	634
	Sc_Est2p	558	F	V	R	S	Q	Y	F	F	N	T	N	T	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	570	
	Ea_p123	631	W	I	M	T	A	Q	I	L	K	R	K	N	I	V	D	S	K	N	F	R	K	E	M	K	D	Y	F	R	Q	K				663

FIG. 42
(CONTINUED)

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A.

Sp_Tip1p	635	F	V	S	E	A	F	S	Y	F	D	M	V	P	F	E	K	V	V	Q	L	S	-	-	M	K	T	S	D	T	L	F	V	665		
Sc_Est2p	571	-	-	-	-	-	-	-	-	-	-	-	V	L	K	L	F	N	V	V	N	A	S	R	-	-	V	P	K	P	Y	E	L	Y	591	
Ea_p123	664	F	Q	K	I	A	L	E	G	Q	Y	P	T	L	F	S	V	L	E	N	E	Q	N	D	L	N	A	K	K	T	L	I	V	696		
Sp_Tip1p	666	D	F	V	D	Y	W	T	K	S	S	S	E	I	F	K	M	L	K	E	H	L	S	G	H	I	V	K	I	G	N	S	Q	Y	698	
Sc_Est2p	592	D	N	V	R	T	V	H	L	S	N	Q	D	V	I	N	V	V	E	M	E	I	F	K	T	A	L	W	V	E	D	K	C	Y	624	
Ea_p123	697	E	A	K	Q	R	N	Y	F	K	K	D	N	L	L	Q	P	V	I	N	I	C	Q	Y	N	Y	I	N	F	N	G	K	F	Y	729	
Sp_Tip1p	699	L	Q	K	V	G	I	P	Q	Q	S	I	L	S	S	F	L	C	H	F	Y	M	E	D	L	I	D	E	Y	L	S	F	T	K	731	
Sc_Est2p	625	I	R	E	D	G	L	F	Q	Q	S	S	L	S	A	P	I	V	D	L	V	Y	D	D	L	L	E	F	Y	S	E	F	K	A	657	
Ea_p123	730	K	Q	T	K	G	I	P	Q	G	L	C	V	S	S	I	L	S	S	F	Y	Y	A	T	L	E	E	S	S	L	G	F	L	R	762	
Sp_Tip1p	732	K	K	G	-	-	-	-	-	-	-	-	S	V	L	L	R	V	V	D	D	F	L	F	I	T	V	N	K	K	D	A	K	K	756	
Sc_Est2p	658	S	P	S	Q	D	-	-	-	-	-	-	T	L	L	K	L	A	D	D	F	L	I	I	S	T	D	Q	Q	V	I	N	I	684		
Ea_p123	763	D	E	S	M	N	P	E	N	P	N	V	N	L	L	M	R	L	T	D	D	Y	L	L	I	T	T	Q	E	N	N	A	V	L	795	
Sp_Tip1p	757	F	L	N	L	S	L	R	G	F	E	K	H	N	F	S	T	S	L	E	K	T	V	I	N	F	E	N	S	N	G	-	-	-	796	
Sc_Est2p	685	I	K	K	L	A	M	G	G	F	Q	K	Y	N	A	K	A	N	R	D	K	I	L	A	V	S	S	Q	S	D	-	-	-	-	713	
Ea_p123	796	F	I	E	K	L	I	N	V	S	R	E	N	G	F	K	F	N	M	K	K	L	Q	T	S	F	F	P	L	S	P	S	K	F	A	828
Sp_Tip1p	787	-	-	-	I	I	N	N	T	F	F	N	E	S	K	K	R	M	P	F	F	G	F	S	V	N	M	R	S	L	D	T	L	L	816	
Sc_Est2p	714	-	-	-	D	D	T	V	I	Q	F	C	A	-	-	M	H	I	F	V	K	E	L	E	V	W	K	H	S	S	T	M	T	M	739	
Ea_p123	829	K	Y	G	M	D	S	V	E	E	Q	N	I	V	Q	D	Y	C	D	W	I	G	I	S	I	D	M	K	T	L	A	L	M	P	861	
Sp_Tip1p	817	A	C	P	K	I	D	E	A	L	F	N	S	T	S	V	E	L	T	K	H	M	G	K	S	F	F	Y	K	I	L	R	S	S	849	
Sc_Est2p	740	N	N	F	H	I	R	S	K	S	S	K	G	I	F	R	S	L	I	A	L	F	N	T	R	I	S	Y	K	T	I	D	T	N	772	
Ea_p123	862	N	I	N	L	R	I	E	G	I	L	C	T	L	N	L	N	M	Q	T	K	K	A	S	M	W										

FIG. 42
(CONTINUED)

A.	Sp_Tip1p	850	L	A	S	F	A	Q	V	F	I	D	I	T	H	N	S	K	F	N	S	C	C	N	I	Y	R	L	G	Y	S	M	C	M	R	882	
	Sc_Est2p	773	L	N	S	T	N	T	V	L	M	Q	I	D	H	V	V	K	N	I	S	E	C	-	-	-	-	-	-	-	-	-	-	-	-	793	
	Ea_p123	895	L	M	N	N	I	T	H	Y	F	R	K	T	I	T	T	E	D	F	A	N	K	T	L	N	K	L	F	I	S	G	G	Y	K	927	
	Sp_Tip1p	883	A	Q	A	Y	L	K	R	M	K	D	I	E	I	P	Q	R	M	F	I	T	D	L	L	N	V	I	G	R	K	I	W	K	K	915	
	Sc_Est2p	794	-	-	-	Y	K	S	A	F	K	D	L	S	I	N	-	-	V	T	Q	N	M	Q	F	H	S	F	L	Q	R	I	I	E	M	821	
	Ea_p123	928	Y	M	Q	C	A	K	E	Y	K	D	H	E	K	K	N	L	A	M	S	S	M	I	D	L	E	V	S	K	I	I	Y	S	V	960	
	Sp_Tip1p	916	L	A	E	I	L	G	Y	T	S	R	R	F	L	S	S	A	E	V	K	W	L	F	C	L	G	M	R	D	G	L	K	P	S	948	
	Sc_Est2p	822	T	V	S	G	C	P	I	T	K	C	D	P	L	I	E	Y	E	V	R	F	T	I	L	N	G	F	L	E	S	L	S	S	N	854	
	Ea_p123	961	T	R	A	F	F	K	Y	L	V	C	N	I	K	D	T	I	F	G	E	E	H	Y	P	D	F	F	L	S	T	L	K	H	F	993	
	Sp_Tip1p	949	F	K	Y	H	P	C	F	E	Q	L	I	Y	Q	F	Q	S	L	T	D	L	I	K	P	L	R	P	V	L	R	Q	V	L	F	981	
	Sc_Est2p	855	T	S	-	-	-	-	-	-	-	-	-	-	-	K	F	K	D	N	I	I	L	L	R	K	E	I	Q	H	L	Q	A	Y	I	877	
	Ea_p123	994	I	E	I	F	S	-	-	-	T	K	K	Y	I	I	F	N	R	V	C	M	I	L	K	A	K	E	A	K	L	K	S	D	Q	C	1023
	Sp_Tip1p	982	L	H	R	R	I	A	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	988		
	Sc_Est2p	878	I	Y	I	H	I	V	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	884		
	Ea_p123	1024	Q	S	L	I	Q	Y	D	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1031		

FIG. 42
(CONTINUED)

B.		
Sp_Tip1p	1	- - - - - MTEHHTPKSRILRFLENQVYVYLCT 24
Sc_Est2p	1	- - - - - - - - - - - MKILFEF 7
Ea_p123	1	MEVDVDNQADNHGIIHSAKTCEEIKEAKTLYSW 33
Sp_Tip1p	25	LNDYVQLVLRGSPA[S]YSNICERLRSDVQTSFS 57
Sc_Est2p	8	IQDKLIDLQTN--STYK--ENLKC GFHNGLD 35
Ea_p123	34	IQKVIRCRNQSQ--SHYK--DLEDIKIFAQTN 61
Sp_Tip1p	58	IFLHSTVVGFDSPKDEGVQFSSPKCSQSELIAN 90
Sc_Est2p	36	EILTTTCFALPNSR-KIALPCLPGDL SHKAVIIDH 67
Ea_p123	62	I VATPRDYNEEDFKVIARKEVFSTGLMIELIDK 94
Sp_Tip1p	91	VVKQMFDESFEERRR-NLLMKGF FSMNHEDFRAMH 122
Sc_Est2p	68	CIIYLLTGELYN--NVLTFFGYK IARNED-- 93
Ea_p123	95	CLVELLSSSDVSDRQKLQCFGFQ LKGNQ-- 122
Sp_Tip1p	123	VNGVQNDLVSTFPNYLISILESKN[W]QLLLEIIG 155
Sc_Est2p	94	- - - VNNSLFCHSANVNVTLLKGA[W]KMFHSLVG 123
Ea_p123	123	- - - LAKTHLLTALSTQKQYFFQDE[W]NQVRAMIG 152
Sp_Tip1p	156	SDAMHY[L]LSKGSIFEALPNDNYLQ[ISG]IPLFKN 188
Sc_Est2p	124	TYAFVD[L]LINYTVIQFN-GQFFTQIVGNRCNEP 155
Ea_p123	153	NELFRH[L]YTKYLI FQRTSEGTLVQFCGNNVFDH 185
Sp_Tip1p	189	NVFEETVSKKRKRRTIETSI TQN--KSARKE[VS] 218
Sc_Est2p	156	HLPKQWVQ--RSSSSSATAAQI--KQLTEPVT 183
Ea_p123	186	LKVNDKFDK-KQKGGAAADMNEPRCCSTCKYN[VK] 217

FIG. 42
(CONTINUED)

B.

Sp_Tip1p	219	WNSISISRFSIFYRSSYKKFKQDLVFNLHSD	251
Sc_Est2p	184	N-----KQFLHKLININSSFFP	200
Ea_p123	218	NEK--DHFLNNINVPNWNMKSRTIRFYCTHFN	248
Sp_Tip1p	252	RNTVHMWLQWIFPRQFGLINAFQVKQLHKV IPL	284
Sc_Est2p	201	-----YSKILPSSS--SICKLTDLREAIFFP	223
Ea_p123	249	R-----NNQFFKKHEFVSNKNNISAMDRAQTI	275
Sp_Tip1p	285	VS-----QSTVVPKRLLKVYPLIEQTAKRLHRIS	313
Sc_Est2p	224	TN-----LVKIPQRLKVRINLTQLKLLKRHKRLN	252
Ea_p123	276	FTNIFRFNRIRKKLKDKVIEKIAMLEKVKDFN	308
Sp_Tip1p	314	LSKVYNHYCPYID-THDDEKILSYSLKPNQ---	342
Sc_Est2p	253	YVSI LNSICPPLEGTVLDLSHL SRQSPKER---	282
Ea_p123	309	FNYYLT KSCPLPENWREKQKIENL INKTREEK	341
Sp_Tip1p	343	-----VFALRSILVRVFPKLI	359
Sc_Est2p	283	-----VLKFIIVILQKLLPQEM	299
Ea_p123	342	SKYYEELFSYTTDNKCVTQFINEFFYNILPKDF	374
Sp_Tip1p	360	WGNQRIFEIILKDL ETFLKL SRYESFSLHYLMS	392
Sc_Est2p	300	FGSKKNKGKIIKNNL LLSLPLNGYLPFDSSLK	332
Ea_p123	375	LTG-RNRKNFQKKVKKYVELNKH ELIHKNNLLE	406
Sp_Tip1p	393	NIKISEIEWLVLGKRSNAKMCLSDFFEKRKQIFA	425
Sc_Est2p	333	KLRKDFRWF LFI S--DIWFTKHNFENLNQLAI	362
Ea_p123	407	KINTREISWMQVETS-AKHFFYYFDHEN-IYVLW	437

FIG. 42
(CONTINUED)

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B.	Sp_Tip1p	426	EF I Y W L Y N S F I I P I L Q S F F Y I T E S S D L R N R T V Y	458
	Sc_Est2p	363	C F I S W L F R Q L I P K I I Q T F F Y C T E I S S T V T - I V Y	394
	Ea_p123	438	K L L R W I F E D L V S L I R C F F Y V T E Q Q K S Y S K T Y Y	470
	Sp_Tip1p	459	F R K D I W K L L C R P F I T S M K M E A F E K I N E N N V R M D	491
	Sc_Est2p	395	F R H D T W N K L I T P F I I V E Y F K T Y L V E N N V C R N H N S	427
	Ea_p123	471	Y R K N I W D V I M K M S I A D L K K E T L A E V Q E K E V E E W	503
	Sp_Tip1p	492	T Q K T T L P P A V I R L L P K K - - N T F R L I T N L R K R F L	522
	Sc_Est2p	428	Y T L S N F N H S K M R I I P K K S N N E F R I I A I P C R G A D	460
	Ea_p123	504	K K S L G F A P G K L R L I P K K - - T T F R P I M T F N K K I V	534
	Sp_Tip1p	523	I K M G S N K K M L V S T N Q T L R P V A S I L K H L I N E - - -	552
	Sc_Est2p	461	E E E - - F T I Y K E N H K N A I Q P T Q K I L E Y L R N K R P T	491
	Ea_p123	535	N S D - - R K T T K L T T N T K L L N S H L M L K T L K N R - M F	564
	Sp_Tip1p	553	E S S G I P F N L E V Y M K L L T F K K D L L K H R M F G R - K K	584
	Sc_Est2p	492	S F T K I Y S P T Q I A D R I K E F K Q R L L K K F N N V L P E L	524
	Ea_p123	565	K D P F G F A V F N Y D D V M K K Y E E F V C K W K Q V G Q P K L	597
	Sp_Tip1p	585	Y F V R I D I K S C Y D R I K Q D L M F R I V K K K L K D P E - F	616
	Sc_Est2p	525	Y F M K F D V K S C Y D S I P R M E C M R I L K D A L K N E N G F	557
	Ea_p123	598	F F A T M D I E K C Y D S V N R E K L S T F L K T T K L L S S D F	630
	Sp_Tip1p	617	V I R K Y A T I H A T S D R A T K N - - - - - - - - - - - - - - -	634
	Sc_Est2p	558	F V R S Q Y F F N T N T G - - - - - - - - - - - - - - - - -	570
	Ea_p123	631	W I M T A Q I L K R K N N I V D S K N F R K K E M K D Y F R Q K	663

FIG. 42
(CONTINUED)

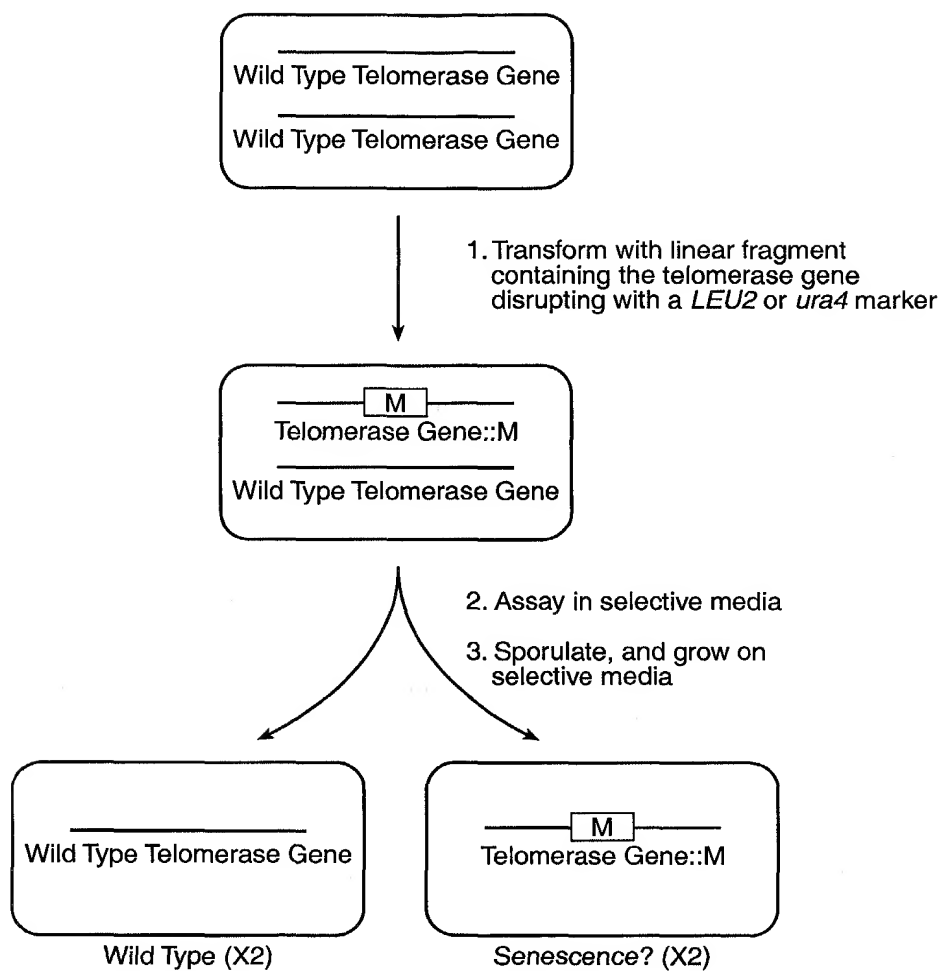
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B.	Sp_Tip1p	635	FVSEAFSYFDMVPFEK	VVQLLS	-	-	MKTS	SDT	L	LFV	665
	Sc_Est2p	571	-	-	-	-	VLKLFNVVNASR	-	-	VPKPYEL	591
	Ea_p123	664	FQKIALEGGQYPTLFS	VLENEQNDLNAKKT	L	I	V				696
	Sp_Tip1p	666	DFVDYWTKSSSEIFKMLKEHLSGH	IVKIGNSQ	Y						698
	Sc_Est2p	592	DNVRTVHL SNQDVINVVEME	IFKTA	LWVEDKCY						624
	Ea_p123	697	EAKQRNYFKKDNLLQPVIN	ICQYNYINFNGK	F	Y					729
	Sp_Tip1p	699	LQKVGIPQGS	SILSFLCHFYMED	LIDEYLS	F	TK				731
	Sc_Est2p	625	IREDGLFQGS	SLSAPIVDLVYDD	LLEFYSEFKA						657
	Ea_p123	730	KQTKGIPQG	LCVSSILSSFYAT	LEEESLGF	L	R				762
	Sp_Tip1p	732	KKG	-	-	-	SVLLRV	VDD	FLFI	TVNKKDAKK	756
	Sc_Est2p	658	SPSQD	-	-	-	TLILKL	ADDFL	IISTD	QQQVIN	684
	Ea_p123	763	DESMNPENPNVNL	MLRLTDDYLL	IIT	TQENNAVL					795
	Sp_Tip1p	757	FLNLSLRGFEKHNF	STSLEK	TVINFEN	SNG	-	-	-		786
	Sc_Est2p	685	IKKLLAMGGFQKYN	AKANRDK	ILAVSSQ	SD	-	-	-		713
	Ea_p123	796	FIEKLINVSRENG	KFNMKK	LQTSFPL	S	PSKFA				828
	Sp_Tip1p	787	-	-	IINN	TFNESKKRMPFF	FGFSVNMR	SLDTLL			816
	Sc_Est2p	714	-	-	DDTV	IQFCA	-	-	MHIFVKE	LEVWKHSSTM	739
	Ea_p123	829	KYGMDSVEEQNI	VQDYCDWIGIS	IDMKT	LALMP					861
	Sp_Tip1p	817	ACP	KIDEALFNSTSV	ELTKHMGKS	FFYK	ILRSS				849
	Sc_Est2p	740	NNFH	IRSKSSKGI	FRSLIALFN	TRISYK	TIDTN				772
	Ea_p123	862	NINLRI	EGILCTLNLN	MQTKKAS	MWLKK	KLKSF				894

FIG. 42
(CONTINUED)

B.	Sp_Tip1p	850	L	A	S	F	A	Q	V	F	I	D	I	T	H	N	S	K	F	N	S	C	C	N	I	Y	R	L	G	Y	S	M	C	M	R	882	
	Sc_Est2p	773	L	N	S	T	N	T	V	L	M	Q	I	D	H	V	V	K	N	I	S	E	C	-	-	-	-	-	-	-	-	-	-	-	-	-	793
	Ea_p123	895	L	M	N	N	I	T	H	Y	F	R	K	T	I	T	T	E	D	F	A	N	K	T	L	N	K	L	F	I	S	G	G	Y	K	927	
	Sp_Tip1p	883	A	Q	A	Y	L	K	R	M	K	D	I	F	I	P	Q	R	M	F	I	T	D	L	L	N	V	I	G	R	K	I	I	W	K	K	915
	Sc_Est2p	794	-	-	-	Y	K	S	A	F	K	D	L	S	I	N	-	-	V	T	Q	N	M	Q	F	H	S	F	L	Q	R	I	I	E	M	821	
	Ea_p123	928	Y	M	Q	C	A	K	E	Y	K	D	H	F	K	K	N	L	A	M	S	S	M	I	D	L	E	V	S	K	I	I	Y	S	V	960	
	Sp_Tip1p	916	L	A	E	I	L	G	Y	T	S	R	R	F	L	S	S	A	E	V	K	W	L	F	C	L	G	M	R	D	G	L	K	P	S	948	
	Sc_Est2p	822	T	V	S	G	C	P	I	T	K	C	D	P	L	I	E	Y	E	V	R	F	T	I	L	N	G	F	L	E	S	L	S	S	N	854	
	Ea_p123	961	T	R	A	F	F	K	Y	L	V	C	N	I	K	D	T	I	F	G	E	E	H	Y	P	D	F	F	L	S	T	L	K	H	F	993	
	Sp_Tip1p	949	F	K	Y	H	P	C	F	F	E	Q	L	I	Y	Q	F	Q	S	L	T	D	L	I	K	P	L	R	P	V	L	R	Q	V	L	F	981
	Sc_Est2p	855	T	S	-	-	-	-	-	-	-	-	-	-	-	-	K	F	K	D	N	I	L	L	R	K	E	I	Q	H	L	Q	A	Y	I	Y	877
	Ea_p123	994	I	E	I	F	S	-	-	-	-	-	-	-	-	-	T	K	K	Y	I	F	N	R	V	C	M	I	L	K	A	K	E	A	K	L	1023
	Sp_Tip1p	982	L	H	R	R	I	A	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	988	
	Sc_Est2p	878	I	Y	I	H	I	V	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	884		
	Ea_p123	1024	Q	S	L	I	Q	Y	D	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1031		

FIG. 42
(CONTINUED)



(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)

FIG. 43

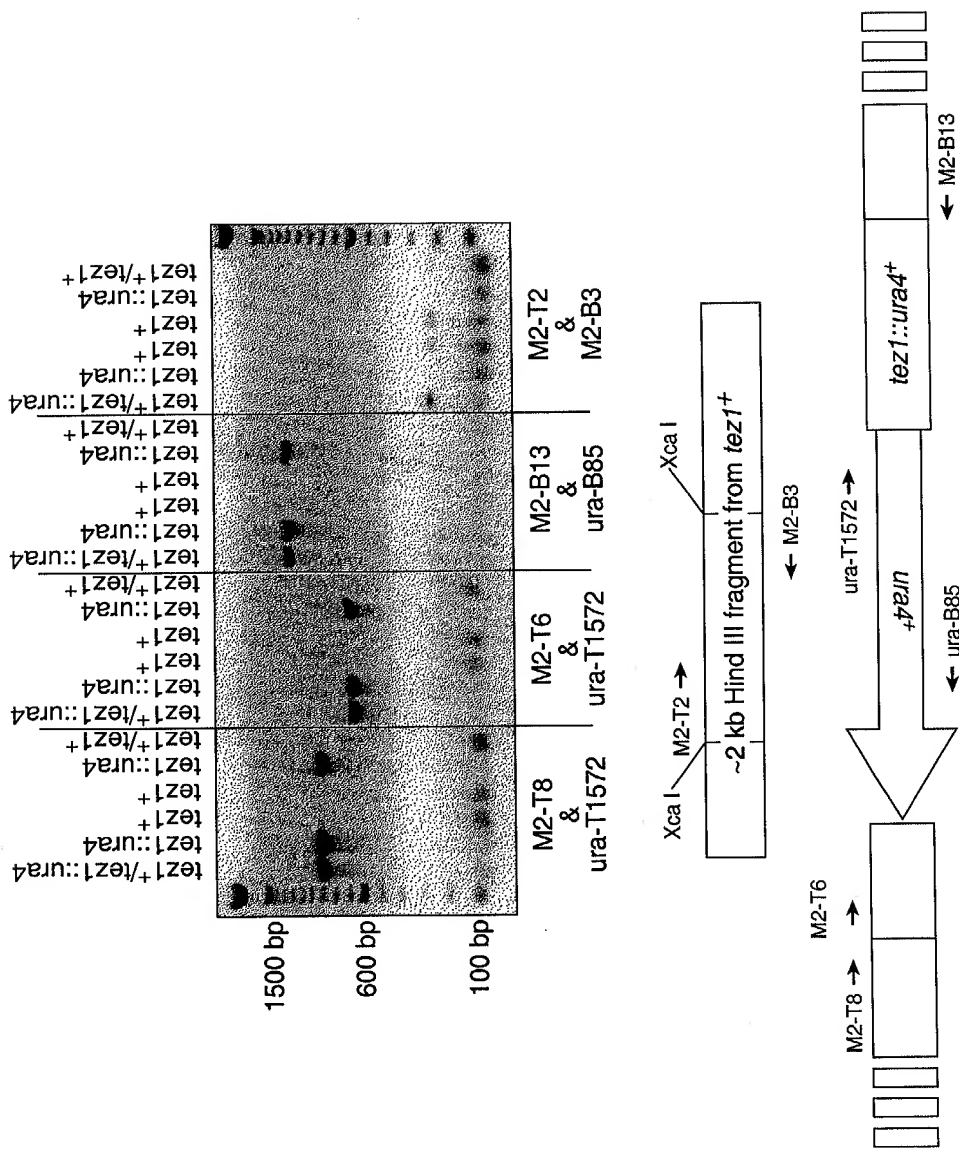


FIG. 44

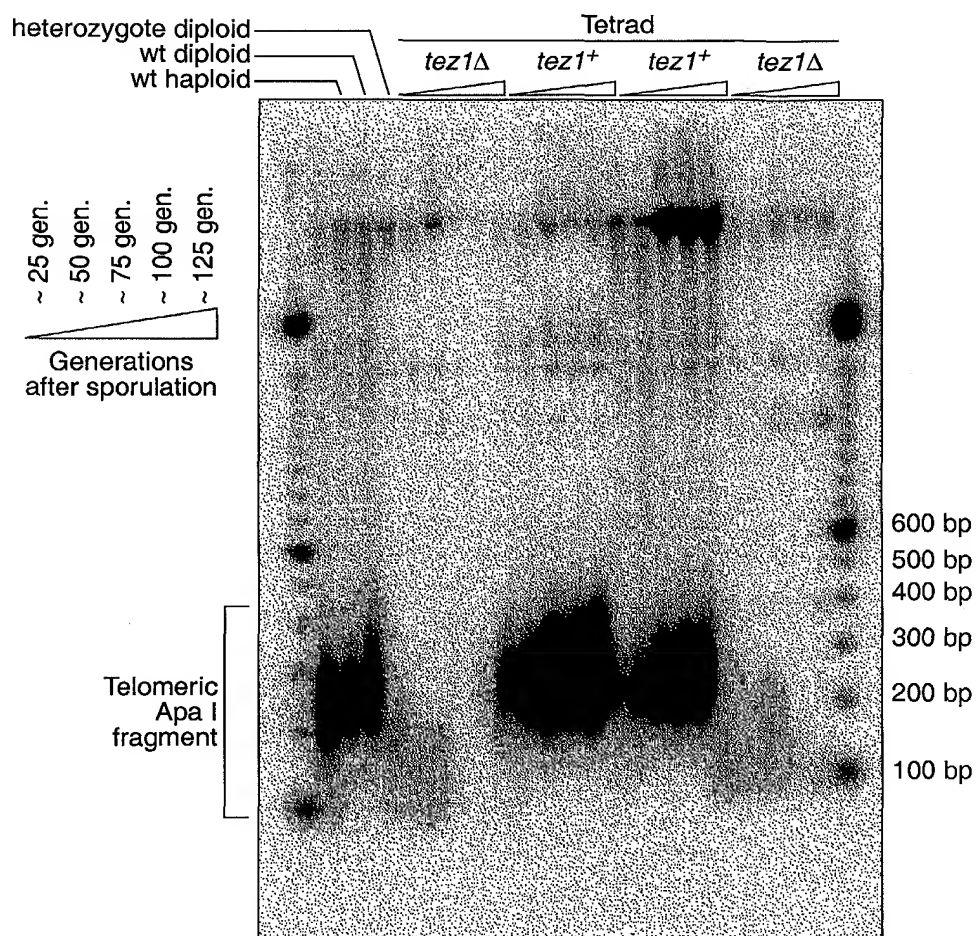


FIG. 45

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FIG. 46

1470 GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA 1529
129 D L V S T F P N Y L I S I L E S K N W Q 148
1530 CTT TTG TTA GAA AT gtaataaccggttaagatgttgcgaacttgaacaagactgacaagtatag T ATC GGC 1601
149 L L L E I 155
1602 AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC 1661
156 S D A M H Y L L S K G S I F E A L P N D 175
1662 AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG 1721
176 N Y L Q I S G I P L F K N N V F E T V 195
1722 TCA AAA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA 1781
196 S K K R K R T I E T S I T Q N K S A R K 215
1782 GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT 1841
216 E V S W N S I S I S R F S I F Y R S S Y 235
1842 AAG AAG TTT AAG CAA G gtaactaataactgtttatccttccataactaatttttag AT CTA TAT TTT AAC 1907
236 K K F K Q D L Y F N 245
1908 TTA CAC TCT ATT TGT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG 1967
246 L H S I C D R N T V H M W L Q W I F P R 265
1968 CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA 2027
266 Q F G L I N A F Q V K Q L H K V I P L V 285
2028 TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA 2087
286 S Q S T V V P K R L L K V Y P L I E Q T 305
2088 GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT 2147
306 A K R L H R I S L S K V Y N H Y C P Y I 325
2148 GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG 2207
326 D T H D D E K I L S Y S L K P N Q V F A 345
2208 TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA 2267
346 F L R S I L V R V F P K L I W G N Q R I 365

FIG. 46
(CONTINUED)

2268 TTT GAG ATA ATA TTA AAA G gttatgtataaaattttattaccactaacgattttaccag AC CTC GAA ACT 2336
 366 F E I I L K D L E T 375

2337 TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TTA ATG AGT AAC ATA AAG 2396
 376 F L K L S R Y E S F S L H Y L M S N I K 395

2397 gtaatatgccaaattttttaccattaattaacaatcag ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA 2465
 396 I S E I E W L V L G 405

2466 AAA AGG TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG 2525
 406 K R S N A K M C L S D F E K R K Q I F A 425

2526 GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCCT TTT TTT TAT 2585
 426 E F I Y W L Y N S F I I P I L Q S F F Y 445

2586 ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA 2645
 446 I T E S S D L R N R T V Y F R K D I W K 465

2646 CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA CGG TTT GAA AAA ATA AAC GAG 2705
 466 L L C R P F I T S M K M E A F E K I N E 485

2706 gtattttaagatattttttgcaaaaagcctaatttttcag AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT 2775
 486 N N V R M D T Q K T 495

2776 ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT ACC TTT CGT CTC ATT ACG 2835
 496 T L P P A V I R L L P K K N T F R L I T 515

2836 AAT TTA AGA AAA AGA TTC TTA ATA AAG gtatttaatttttggtcacatcaatgtacttttacttctaatctatta 2906
 516 N L R K R F L I K 524

2907 ttagcag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG 2967
 525 M G S N K K M L V S T N Q T L R P V 542

2968 GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG 3027
 543 A S I L K H L I N E E S S G I P F N L E 562

3028 GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gtaat 3088
 563 V Y M K L L T F K K D L L K H R M F G 581

FIG. 46
(CONTINUED)

3089	tataaatgcgcgattcctcattattaatttcag	G	CGT	AAG	AAG	TAT	TTT	GTA	CGG	ATA	GAT	ATA	3155								
582		R	K	K	Y	F	V	R	I	D	I	591									
3156	AAA	TCC	TGT	TAT	GAT	CGA	ATA	AAG	CAA	GAT	TTG	ATG	TTT	CGG	ATT	GTT	AAA	AAG	AAA	CTC	3215
592	K	S	C	Y	D	R	I	K	Q	D	L	M	F	R	I	V	K	K	L	611	
3216	AAG	GAT	CCC	GAA	TTT	GTA	ATT	CGA	AAG	TAT	GCA	ACC	ATA	CAT	GCA	ACA	AGT	GAC	CGA	GCT	3275
612	K	D	P	E	F	V	I	R	K	Y	A	T	I	H	A	T	S	D	R	A	631
3276	ACA	AAA	AAC	TTT	GTT	AGT	GAG	CGG	TTT	TCC	TAT	T	gtaagttattatttttttcattggaattttttaacaa	3343							
632	T	K	N	F	V	S	E	A	F	S	Y	F	643								
3344	attcttttttag	TT	GAT	ATG	GTG	CCT	TTT	GAA	AAA	GTC	GTG	CAG	TTA	CTT	TCT	ATG	AAA	ACA	3405		
644		D	M	V	P	F	E	K	V	V	Q	L	L	S	M	K	T	659			
3406	TCA	GAT	ACT	TTG	TTT	GTT	GAT	TTT	GTG	GAT	TAT	TGG	ACC	AAA	AGT	TCT	TCT	GAA	ATT	TTT	3465
660	S	D	T	L	F	V	D	F	V	D	Y	W	T	K	S	S	E	I	F	679	
3466	AAA	ATG	CTC	AAG	GAA	CAT	CTC	TCT	GGA	CAC	ATT	GTT	AAG	gtataccaattgttgaaattgtaataaca	3532						
680	K	M	L	K	E	H	L	S	G	H	I	V	K	692							
3533	ctaataagaactag	ATA	GGA	AAT	TCT	CAA	TAC	CTT	CAA	AAA	GTT	GGT	ATC	CCT	CAG	GGC	TCA	3593			
693		I	G	N	S	Q	Y	L	Q	K	V	G	I	P	Q	G	S	708			
3594	ATT	CTG	TCA	TCT	TTT	TTG	TGT	CAT	TTT	TAT	ATG	GAA	GAT	TTG	ATT	GAT	GAA	TAC	CTA	TCG	3653
709	I	L	S	S	F	L	C	H	F	Y	M	E	D	L	I	D	E	Y	L	S	728
3654	TTT	ACG	AAA	AAG	AAA	GGA	TCA	GTG	TTG	TTA	CGA	GTA	GTC	GAT	TTT	ATA	ACA	3713			
729	F	T	K	K	K	G	S	V	L	L	R	V	V	D	D	F	L	F	I	T	748
3714	GTT	AAT	AAA	AAG	GAT	GCA	AAA	AAA	TTT	TTG	AAT	TTA	TCT	TTA	AGA	G	gtgagttgctgtcattcc	3777			
749	V	N	K	K	D	A	K	K	F	L	N	L	S	L	R	G	764				
3778	taagttctaaccgttgag	GA	TTT	GAG	AAA	CAC	AAT	TTT	TCT	ACG	AGC	CTG	GAG	AAA	ACA	GTA	3840				
765		F	E	K	H	N	F	S	T	S	L	E	K	T	V	778					
3841	ATA	AAC	TTT	GAA	AAT	AGT	AAT	GGG	ATA	ATA	AAC	AAT	ACT	TTT	TTT	AAT	GAA	AGC	AAG	AAA	3900
779	I	N	F	E	N	S	N	G	I	I	N	N	T	F	F	N	E	S	K	K	798

FIG. 46
(CONTINUED)

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[illegible]

FIG. 46
(CONTINUED)

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4666 gctgaccccccaagcaagcatactataggatttcttagtaagtaaaataatctcgttattagttttgacttgct 4745
4746 ttatccttatacttttaagaaagattgacagtggttgctgactactgcccacatgccattaaacgggagtggttaaca 4825
4826 ttaaaagtaatacatgaggttaactcctttcatttagaataaggaagtgtttctataatgaataatgccgcacta 4905
4906 atgcaaaaagacgaagattatcttcaacaagggtgattagcatatccgaaggaaagagtaataatccccagttt 4985
4986 gttgaagaaagcaaggataatttggaacaagcttctgcagatgacaggctaaattttggtgaccgaattttggtaaaagc 5065
5066 cccaggttatccatggtgcccgttctgactgagacgaaagaaactaagtagtttgaaactactaatagctcattta 5145
5146 atgtcttataaagggtttgtttttctgacttcaattttgcatgggtgaaagaaatagtggttaagccattattggat 5225
5226 tccgaatatagccaaatttctggttcccaagggaagtctaaagaacttattgaagcttatgaggttcaaaactcc 5305
5306 tcctgatttaaggagggaatcttccaccgatgaggaaatggatagcttatcagctgctgagagagcctaatttttgc 5385
5386 aaaaaagaaaatatcatctggagagacatctcttgatgaatcagatcgagagatctccagggatccttgatgtcaata 5465
5466 acttctatttctgaaatgtatggtcctactgtcgtctcgtactctcgtagcttaagtgacccaaagggtacc 5544

FIG. 46
(CONTINUED)

1
 met ser val tyr val val glu leu leu
 ATG AGT GTG TAC GTC GTC GAG CTG CTC
 GCCAAGTTCCTGCACTGGCTG
 10
 arg ser phe phe tyr val thr glu thr thr phe gln lys asn arg
 AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG
 20
 30
 leu phe phe tyr arg lys ser val trp ser lys leu gln ser ile
 CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT
 40
 gly ile arg gln his leu lys arg val gln leu arg glu leu ser
 GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG TCG
 50
 60
 glu ala glu val arg gln his arg glu ala arg pro ala leu leu
 GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG CTG
 70
 thr ser arg leu arg phe ile pro lys pro asp gly leu arg pro
 ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG CCG
 80
 90
 ile val asn met asp tyr val val gly ala arg thr phe arg arg
 ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC AGA
 100
 glu lys ala glu arg leu thr ser arg val lys ala leu phe
 GAA AAG ARG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG TTC
 110
 120
 ser val leu asn tyr glu arg ala arg arg pro gly leu leu gly
 AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG GGC
 130
 140
 ala ser val leu gly leu asp asp ile his arg ala trp arg thr
 GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC ACC
 150
 phe val leu arg val arg ala gln asp pro pro pro glu leu tyr
 TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG TAC
 160
 170
 phe val lys val asp val thr gly ala tyr asp thr ile pro gln
 TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC CAG
 180
 asp arg leu thr glu val ile ala ser ile ile lys pro gln asn
 GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC
 190
 200
 thr tyr cys val arg arg tyr ala val val gln lys ala ala met
 ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC ATG

FIG. 47

210
 gly thr ser ala arg pro ser arg ala thr ser tyr val gln cys
 GGC ACG TCC GCA AGG CCT TCA AGA GCC ACG TCC TAC GTC CAG TGC
 220
 gln gly ile pro gln gly ser ile leu ser thr leu leu cys ser
 CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC
 230
 240
 leu cys tyr gly asp met glu asn lys leu phe ala gly ile arg
 CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG ATT CGG
 250
 arg asp gly leu leu leu arg leu val asp asp phe leu leu val
 CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG TTG GTG
 260
 270
 thr pro his leu thr his ala lys thr phe leu arg thr leu val
 ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC CTG GTC
 280
 arg gly val pro glu tyr gly cys val val asn leu arg lys thr
 CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG AAG ACA
 290
 300
 val val asn phe pro val glu asp glu ala leu gly gly thr ala
 GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC ACG GCT
 310
 phe val gln met pro ala his gly leu phe pro trp cys gly leu
 TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC GGC CTG
 320
 330
 leu leu asp thr arg thr leu glu val gln ser asp tyr ser ser
 CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC TCC AGC
 340
 tyr ala arg thr ser ile arg ala ser leu thr phe asn arg gly
 TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC CGC GGC
 350
 360
 phe lys ala gly arg asn met arg arg lys leu phe gly val leu
 TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG GTC TTG
 370
 arg leu lys cys his ser leu phe leu asp leu gln val asn ser
 CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC
 380
 390
 leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln
 CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG
 400
 ala tyr arg phe his ala cys val leu gln leu pro phe his gln
 GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG
 410

FIG. 47
(CONTINUED)

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420
gln val trp lys asn pro his phe ser cys ala ser ser leu thr
CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

430
arg leu pro leu leu leu his pro glu ser gln glu arg arg asp
CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

440
arg leu pro leu leu leu his pro glu ser gln glu arg arg asp
CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

450
val ala gly gly gln gly arg arg arg pro ser ala leu arg gly
GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

460
arg ala val ala val pro pro ser ile pro ala gln ala asp ser
CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

470
arg ala val ala val pro pro ser ile pro ala gln ala asp ser
CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

480
thr pro cys his leu arg ala thr pro gly val thr gln asp ser
ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

490
pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys
CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

500
pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys
CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

510
pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp
CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

520
his pro gly leu met ala thr arg pro gln pro gly arg glu gln
CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

530
his pro gly leu met ala thr arg pro gln pro gly arg glu gln
CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

540
thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly
ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG

550
arg gly gly pro his pro gly leu his arg trp glu ser glu ala
AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

560
arg gly gly pro his pro gly leu his arg trp glu ser glu ala
AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

564
OP
TGA GTGAGTGTGTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCG
CTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCGTTTTCACTTCCCCAC
AGGCTGGCGTTCGGTCCACCCAGGGCCAGCTTTTCTCACCAGGAGCCCGGCTTCCACT
CCCCACATAGGAATAGTCCATCCCCAGATTGCCATTGTTTACCCTTCGCCCTGCCTTCC
TTTGCCTTCCACCCCCACCATTTCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTTTGGG
AATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGG
GTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAATACTGAATATATGAGTT
TTTCAGTTTTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIG. 47
(CONTINUED)

$$+$$

Motif -1
 Ep p123 ...LVVSLIRCFFYVTEQQKSYSKT...
 Sp Tez1 ...FIIPILQSFFYITESDLNRNT...
 Sc Est2 ...LIPKIIQTFFYCTEISSTVTIV...
 Hs TCP1 ...YVVELLRSFFYVTETTFQKNRL...
 consensus FFY TE

Motif 0
 Ep p123 ...KSLGFAPGKLRLIPKKT--TFRPIMTFNKKIV...
 Sp Tez1 ...QKTTLPPAVIRLLPKKN--TFRLITNLRKRFL...
 Sc Est2 ...TLSNFNHSMRIIPKKSNEFRIIAIPCRGAD...
 Hs TCP1 ...ARPALLTSRLRFIPKPD--GLRPVNMMDYVVG...
 consensus R PK R I

Motif A
 Ep p123 ...PKLFFATMDIEKCYDSVNREKLSTFLK...
 Sp Tez1 ...RKKYFVRIDIKSCYDRIKQDLMFRIVK...
 Sc Est2 ...PELYFMKFVDVKSCYDSIPRMECMRILK...
 Hs TCP1 ...PELYFVKVDVTGAYDTIPQDRLTEVIA...//...
 consensus F D YD

Motif B
 Ep p123 ...NGKFKYQTKGIPQGLCVSSILSSFYYA...
 Sp Tez1 ...GNSQYLQKVGIPQGSILSSFLCHFYE...
 Sc Est2 ...EDKCYIREDGLFQGSSLSAPIVDLVYD...
 Hs TCP1 ...RATSYVQCQGIPQGSILSTLLCSLCYG...
 consensus G QG S

Motif C
 Ep p123 ...PNVNLLMRLTDDYLLITTQENN...
 Sp Tez1 ...KKGSVLLRVVDDFLFITVNKKD...
 Sc Est2 ...SQDTLILKLADDFLIISTDQQQ...
 Hs TCP1 ...RRDGLLLRLVDDFLLVTPHLTH...
 consensus DD L

Motif D
 Ep p123 ...NVSRENGFKFNMKKL...
 Sp Tez1 ...LNLSLRGFEEKHNFST...
 Sc Est2 ...KKLAMGGFQKYNAKA...
 Hs TCP1 ...LRTLVRGVPEYGCVV...
 consensus G

FIG. 48